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AF149721 Homo sapi
AF024401 Homo sapi
AF024401 Homo sapi
AF17756 Mus muscu
AF17755 Mus muscu
AC124608 Mus muscu
AC126996 Rattus no
AC125534 Rattus no
AR037594 Homo sapi
AF149722 Homo sapi
AX367043 Sequence
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AF062748 Homo sapi
AC107214 Homo sapi
AC107214 Homo sapi
AC122966 Rattus no
AC128348 Rattus no
AC129658 Rattus no
AC124017 Xenopus 1
AC144762 Homo sapi
AB098919 Bos tauru
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AF053537 Homo sapi
BC030128 Homo sapi
AJ006851 Homo sapi
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AF078835 Homo sapi
AJ310392 Homo sapi
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-DE-Gen2 1/USFTO spool p/US09513365/runat_12012004_163932_28772/app_query.fasta_1.455
-DE-GENEMD1 -QFWT=fastap -SUFFIX=pln.rge -MINMATCH=0.1 -LOOPEL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-UNITS=bits -START=1 -END=-1 -MATRIX=bund=15 -MODE=LOCAL
-OUTHWT=ptc -NORM=ext -HEAFSIZE=560 -MINLEN=0 -MAXLEN=200000000
-USER=US09513365 @CGN 1 1 4958 @runat_12012004_163932_28772 -NCPU=6 -ICPU=3
-NO WMAP -LARGEQUERY -NGG SCORES=0 -MAXLT -DSPBLACK=160 -LONGLOG
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                                                                                                                                  Summada, Y., Saito, A. and Horie, M.

Shimada, Y., Saito, A. and Horie, M.

Direct Submission

Submitted (07-APR-1998) Yoshikazu Shimada, Otsuka Pharmaceutical
Co. Ltd., Otsuka GEN Research Institute; Kagasuno, Kawauchi-cho,
Tokushima, Tokushima 771-0192, Japan

(E-mail:shim@csuka.genome.ad.jp, Tel:81-886-65-2888 (ex.2476),
Pax:81-886-37-1035)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Shimada,Y., Saito,A., Suzuki,M., Takahashi,E. and Horie,M.
Cloning of a novel gene (ING1L) homologous to ING1, a candidate
                                                                                                                                                                                                                                                                             261 AspasnGluLysThrMetAspLysSerThrGluLysThrLysLysBaspArgArgSerArg
                                                                                                                                                                                      LysLysSerLysSerAlaLysLysLysLysArgSerLysAlaLysGlnGluArgGluAla
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                                                                                                                                                                          SerTyrGlyGluMetIleGlyCysAspAsnGluGlnCysProIleGluTrpPheHisPhe
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AB012853
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        tumor suppressor
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99172097
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Location/Qualifiers
1. .1078
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Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                           PRI 15-AUG-2001
                                                                                                                                                                      261 AspAsnGluLysThrMetAspLysSerThrGluLysThrLysLysAspArgSerArg 280
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1080)
                                                                                      668 TCACCTGTTGAGTTTGCAATAGATCCTAATGAACCTACATACTGCTTATGCAACCAAGTG
                                                                                                                                                                                                                                                                                     GATAATGAGAAAACAATGGACAAAAGTACTGAAAAGACAAAAAAGGATAGAAGATCGAGG
      SerProValGluPheAlaIleAspProAsnGluProThrTyrCysLeuCysAsnGlnVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nagashima, M., Shiseki, M., Miura, K., Hagiwara, K., Linke, S.P., Pedeux, R., Wang, X.W., Yokota, J., Riabowol, K. and Harris, C.C. DNA damage-inducible gene p331NG2 negatively regulates cell proliferation through acetylation of p53 Proc. Natl. Acad. Sci. U.S.A. 98 (17), 9671-9676 (2001) 21396501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission (12-MAR-1998)
Nagadafilma, M., Hagiwara, K., Minter, A.R. and Harris, C.C.
Nagadafilma, M., Hagiwara, K., Minter, A.R. and Harris, C.C.
Submitted (12-MAR-1998) Laboratory of Human Carcinogenesis,
National Cancer Institute, 37 Convent Drive Bldg.37 Rm.2C01.
Bethesda, MD 20892, USA
Location/Qualifiers
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Homo sapiens p33 (ING2) mRNA, complete cds.
AF053537
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Matches:
Conservative:
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| map="4435"
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196 c 271 g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    248 AAGGAAATTGATGATGTCTACGAAAATATAAGAAAGAAGAAGATGATTTAAACCAGAAGAAA 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ArgLeuGlnGlnLeuLeuGlnArgAlaLeuIleAsnSerGlnGluLeuGlyAspGluLys 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 308 CGTCTACAGCAGCTTCTCCAGAGAGCACTAATTAATAAGTCAAGAATTGGGAGAGATGAAAAA
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                                                                                                                                                                                               1
Harris,C.C. and Nagashima,M.
Tumour suppressor gene, p47ing3
Parent: WO 0159114-A 7 16-AUG-2001;
THE SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES
Location/Qualifiers
                                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Butelo
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo
      linear
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Matches:
Conservative:
Mismatches:
Indels:
        DNA
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                                                                  AX211560.1 GI:15523814
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Homo sapiens
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Contact: MGC help desk

Contact: MGC help desk

Email: Gagabs-Temail.nih.gov

Tissue Procurement: DCTD/DTP

Tissue Procurement: DCTD/DTP

Tissue Procurement: DCTD/DTP

CDNA Library Preparation: Rubin Laboratory

CDNA Library Preparation: Rubin Laboratory

CDNA Library Preparation: Rubin Laboratory

CDNA Library Preparation:

DNA Sequencing by: National Institutes of Health Intramural

Sequencing Center (NISC)

Gaithersburg, Maryland;

Web Sate: http://www.nisc.nih.gov/

Contact: nisc mgc@nhgri.nih.gov/

Contact: nisc mgc@nhgri.nih.gov/

Contact: nisc mgc@nhgri.nih.gov/

Contact: N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,

Blakesley,R.W., Bouiffard,G.G., Breen,K., Britley,C., Brooks,S.,

Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P.,

Masiello,C., Maskeri,B., Mastrian,S.D.,McCloskey,J.C., McDowell,J.,

Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W., Tsurgeon,C.,

Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L., Young,A.,

Zhang,L.-H. and Green,E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /translation="MGQQQQQLYSSAALLTGERSRLLTCYVQDYLECVESLPHDMQR
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RDLCHMANGIEDCDDQPPKSKKSKAKKKRSKAKQBREAS9VBFAIDPNBFYYCLCN
QVSYGEMIGCDNEQCPIEWFHFSCVSLTYKFKGKWYCPKCRGDNEKTMDKSTEKTKKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Clone distribution: MGC clone distribution information can be foun through the I.M.A.G.B. Consortium/LLNL at: http://image.llnl.gov Series: IRAL Plate: 15 Row: m Column: 11
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 4504694.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21 SerArgLeuLeuThrCysTyrValGlnAspTyrLeuGluCysValGluSerLeuProHis 40
                                                                                   Submitted (07-MAY-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive; Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              136 ATGTTAGGGCAGCAGCAGCAGCAACTGTACTCGTCGGCTGCGCTCCTGACCGGGGAGCGG
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/product="inhibitor of growth family, member 1-like"
/protein_id=AAH30128.1"
/db_xref="G1:20987213"
      Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /tissue type="Lung, small cell carcinoma"
/clone lib="NIH MGC 7"
/lab host="DH10B-R"
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/mol_type="mRNA"
/db_xref="LocusID:3622"
/db_xref="taxon:9606"
/clone="MGC:10524 IMAGE:3941655"
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Mismatches:
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Strausberg, R.
Direct Submission
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                  SerArgLeuLeuThrCysTyrValGlnAspTyrLeuGluCysValGluSerLeuProHis
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  Mismatches:
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/ gene="ing2"
/ codon start=1
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QVSYGEMIGGDNEQCPIEWFHFSGVSLTYKPKGKWYCPKCRGDNEKTMDKSTEKTKKD
RRSR."
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Homo sapiens mRNA for p32 protein.
AJ006851.
GI:12053587
ing2 gene; p32 protein.
Homo sapiens (human)
AGCCGGCTGCTACCTGCTACCTGCAGGACTACCTTGAGTGCGTGGAGTCGCTGCCCCAC
                                                             GACATGCAGAGGAACGTGTCTGTGCTGCGAGAGCTGGAACAACAAATATCAAGAAACGTTA
                                                                                                         LysGluIleAspAspValTyrGluLysTyrLysLysGluAspAspLeuAsnGlnLysLys
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Submitted (08-JUN-1998) Lopez-Otin C., Bioquimica y Biologia
Molecular, Universidad de Oviedo. Facultad de Medicina., C/ J
Claveria s/n., 33066, SPAIN
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cal,S., Freije,J.M. and Lopez-Otin,C.
ING2,a new possible gene supressor tumor
Unpublished
                                              AspMetGlnArgAsnVal
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RNVSVLRELDNKYQETLKEIDDVYEKYKKEDDSNQKKRLQQHLQRALINSQELGDEKI
QIVTQMLELVENRARQMELHSQCFQDPAESERASDKSKMDSSQPERSSRRPKRQRTSE
                                                                                                                                                        SRDLGHMTNGI DDCDDQPPKEKRSKSAKKKRSKAKQEREASPVEFAI DPNEPTYCLC
NQVSYGEMI GCDNEQCPI EWFHFSCVSLTYKPKGKWY CPKCRGDNEKTMDKSTEKTKK
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           product="Similar to inhibitor of growth family, member
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: MGC help desk
Email: cgapbs-remail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing Center (NISC),
Gaithersburg, Maryland;
Web site: http://www.nisc.nih.gov/
Contact: nisc mgc@nhgri.nih.gov/
Contact: nisc mgc@nhgri.nih.gov/
Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P.,
Hansen,N., Mo.S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R.,
Maduro,Q.L., Masiello,C., Maskeri,B., Mastrian,S.D., McCloskey,J.C.,
McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,
Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,
Young,A., Zhang,L.-H. and Green,E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Clone distribution: MGC clone distribution information can be found through the I.M.A.G.B. Consortium/LINL at: http://image.llnl.gov Series: IRAK Plate: 108 Row: o Column: 20 This clone was selected for follength sequencing because it passed the following selection criteria: matched mRNA gi: 12963706. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                     linear ROD OL-MEN. C.L.
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
1 (bases 1 to 1262)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submitseion
Submitted (31-MAR-2003) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
SerCysValSerLeuThrTyrLysBroLysGlyLysTrpTyrCysProLysCysArgGly
                                                                                                                                                                            AspAsnGlulysThrMetAspLysSerThrGluLysThrLystysAspArgSerArg
                                                                  SerTyrGlyGluMetIleGlyCysAspAsnGluGlnCysProIleGluTrpPheHisPhe
                                                                                              TCTTATGGGGAGATGATGATGATGAATGAATGAACAGTGTCCAATTGAATGGTTTCACTTT
                                                                                                                                                                                                                                                                                 GATAATGAGAAACAATGGACAAAAGTACTGAAAAGACAAAAAAGGATAGAAGATCGAGG
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Mus musculus, Similar to inhibitor of growth
clone IMAGE:6515125, mRNA, partial cds.
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old mouse. Taken by biopsy."
/clone_lib="NCI_CGAP_Mam2"
/lab_host="DH10B"
/note="Vector: pCMV-SPORT6"
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/clone="IMAGE:6515125"
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/strain="FVB/N-3"
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AAACGCCTACAGCAGCATCTCCAGAGAGCGTTAATCAATAGCCAAGAATTGGGAGATGAA 307
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                                    LysileGlnIleValThrGlnMetLeuGluLeuValGluAsnArgAlaArgGlnMetGlu
                                                                      AAAATTCAGAATGTCACCCAGATGCTCGGATTGGTGGAGAACCGATCGAGACAAATGGAG
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Jones, K.A., Volkmuth, W. and Walker, M.G.
Bone remodeling genes
Patent: US 6426186-A 81 30-JUL-2002;
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I (Dases 1 to 1001)

Nagashima,M., Hagiwara,K., Hancock,A.R. and Harris,C.C.

Direct Submission

Submitted (16-JUL-1998) Laboratory of Human Carcinogenesis,

National Cancer Institute, National Institutes of Health, 37

Convent Dr., Bldg, 37, Rm. 2C01, Bethesda, MD 20892, USA

Location/Qualifiers

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Aprice (Ab_xref="mand" mesculus" mesculus" mol. type="mand" mesculus" mol. type="mand" mesculus" mol. type="mand" 
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Mus musculus p331NG2 (Ing2) mRNA, complete cds.
AF078834
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VERSION AF062748.1 GI:9992841 KEYWORDS SEGMENT 2 of 2 SOURCE Homo sapiens (human) ORGANISM Homo sapiens (human) ORGANISM Homo sapiens Eucharyota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae, Homo. Mammalia; Luberia; Primates; Catarrhini; Hominidae, Homo. AUTHORS Nagashima,M., Hagiwara,K., Minter,A.R. and Harris,C.C. TITLE Joinect Submission JOURNAL Submitted (01-MAY-1998) Laboratory of Human Carcinogenesis, National Cancer Institute, 37 Convent Dr. Bldg.37, Rm.2C26, Rethesda. MD 20892, 115A	Decation Decation	/ De xref=01:99918120.1 / Ab xref=01:99918120.1 / translation="WLGQQQQQLYSSAALLTGERSRLLTCYVQDYLECVESLPHDMQR NVSYLRELDWYVEXFEXTEDDLWXGFRALLNGGELGDEKIQ IVTOWLELVENRARQWELESCPCPDPAESERASDRAKMDSSGPERSERPRRGRISSE RDLCHWANGIEDCDDQPPKEKKSKSAKKRRSKAKQEREASPVEFAIDPNEFTYCLCN QVSYCEMIGCDNEQCPIEWFHFSCVSLTYKPKGKWYCPKCRGDNEKTMDKSTEKTKKD RRSR" / Gree="ING2" / number=1 exon	Alignment Scores:	11
	Db 187 TGTGCCGGGGGCGTTGGTTCGGCCCCAGCGAGTCCGAATCGGGGTTTGCAGCATGTTTT 246 Qy 57		SARGSELLyshlaLysGlnGluArgGluAlaSerProvalGluPheAlaIleAspProAs 21	250 #G1VLV#TrpTyrCysProLysCysArgG1yAspAsnG1uLy#ThrMetAspLysSerTh

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Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see http://genome.wustl.edu/gsc
                                                                                                                                      USA
St. Louis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NOTICE: This sequence may not represent the entire insert of this fone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 0); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOURCE INFORMATION:
The RPCI-11 human BAC library was made from the blood of one male donor, as described by 90 socgawa, K., Woon, P.Y., Zhao, B., Frengen, E. Tateno, M., Catanese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong and coworkers at http://www.chori.org
                                                                                                                                                                                                                             Submitted (15-OCT-2002) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, On Sep 20, 2002 this sequence version replaced gi:20128734.
                                                                                                              Washington
Missouri 63108,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              There is an unresolved tandem repeat from base 87660 to 89441,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This sequence was finished as follows unless otherwise noted:
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                                                                                                                                                                                                                                                                                                               Center: Washington University Genome Sequencing Center
Center code: WUGSC
University School of Medicine, 4444 Forest Park Parkway,
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Location/Qualifiers
1. .183317
                                                                                                              Department of Genetics,
Park Avenue, St. Louis,
                                                                                                                                                                                                                                                                                                                                                                 Web site: http://genome.wustl.edu/gsc
Contact: sapiens@watson.wustl.edu
------ Summary Statistics
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/db_xref="taxon:9606"
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                                                                                                                                 University, 4444 Forest 7 (bases 1 to 183317)
                                                                                         Direct Submission
Submitted (03-OCT-2002)
                     MO 63108, USA
6 (bases <u>1</u> to 183317)
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Homo sapiens BAC clone RP11-367N14 from 4, complete sequence.
AC107214
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University School of Medicine, 4444 Forest Park Parkway, St. Louis,
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Catarrhini; Hominidae; Homo.
                         285 GAAAATCGGGCAAGACAAATGGAGTTACACACTCACAGTGTTTCCAAGATCCTGCTGAAAGT
                                                                                                                                      345 GAACGAGCCTCAGATAAAGCAAAGATGGATTCCAGCCAACCAGAAAGATCTTCAAGAAGA
                                                                                                                                                                                                                                                                          SerLysAlaLysGlnGluArgGluAlaSerProValGluPheAlaIleAspProAsnGlu
                                                                                                                                                                                                                                                                                                                                                                                           ProThrTyrCysLeuCysAsnGlnValSerTyrGlyGluMetIleGlyCysAspAsnGlu
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                                                                                                                                                                                     ProArgArgGlnArgThrSerGluSerArgAspLeuCysHisMetAlaAsnGlyIleGlu
  GluAsnArgAlaArgGlnMetGluLeuHisSerGlnCysPheGlnAspProAlaGluSer
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licine, 4444 Forest Park Parkway, St.
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Submitted (20-SEP-2002) Genome Sequencing Center, Washington
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Nguyen,C., Haglund,K. and Spalding,L.
The sequence of Homo sapiens BAC clone RP11-367N14
Upublished (2001)
3 (bases 1 to 183317)
Waterston,R.H.
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Genome Res. 8 (11), 1097-1108 (1998)
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Mammalla, Eutheria, Primates;
1 (Dases 1 to 183377)
Sulston, J.E. and Waterston, R.
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Waterston, R.H.
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Homo sapiens
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Submitted (07-MAR-2003) Whitehead Institute/MIT Center for Genome
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Center: Whitehead Institute/ MIT Center for Genome Research
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            Research, 320 Charles Street, Cambridge, MA 02141, USA On Mar 7, 2003 this sequence version replaced gi:28195970. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                     Center Clone name: 296_C_23
Sequencing vector: Plasmid; n/a; 100% of reads Sequencing vector: Plasmid; n/a; 100% of reads Chemietry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.960731
Consensus quality: 191671 bases at least Q30
Consensus quality: 192003 bases at least Q30
Consensus quality: 192003 bases at least Q20
Insert size: 188000; agarose-fp
Insert size: 188000; agarose-fp
Quality coverage: 9.1 in Q20 bases; sum-of-contigs
Quality coverage: 8.9 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2597: contig of 2597 bp in length 2697: gap of 100 bp 2530: contig of 2433 bp in length 5230: gap of 100 bp 91253: contig of 86023 bp in length 91253: contig of 10990 bp in length 102443: gap of 100 bp 135243: contig of 10900 bp in length 135243: contig of 54928 bp in length 190371: contig of 54928 bp in length 190371: gap of 100 bp 190371: gap of 100 bp 190371: gap of 100 bp 190371: contig of 5382 bp in length 19273: contig of 5382 bp in length.
                                                                                                                                                                                                                   Web site: http://www-seq.wi.mit.edu
Contact: sequence submissions@genome.wi.mit.edu
------ Project Information
Center project name: 119778
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1. .2597
/note="assembly_fragment
clone_end:SP6
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2698. .5130
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190372. 192753
/note="assembly_fragment
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/db_xref="taxon:10090"
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                                                        AC107236 192753 bp DNA linear HTG 07-MAR-2003
Mus musculus clone RP23-296C23, WORKING DRAFT SEQUENCE, 7 unordered
                            252 LysTrpTyrCysProLysCysArgGlyAspAsnGluLysThrMetAspLysSerThrGlu 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                  45851 AAGACAAAAAGGATAGAAGATCGAGG 45877
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                                                                                                                              LysThrLysLysAspArgArgSerArg 280
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Mus musculus (house mouse)
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Marany, Danales, Hocksker, M.Lee., Abramazon, S., Adams, C., Alder, J., Allen, H., Alsbarocks, S., Amin, A., Angulano, D., Angales, I. Co., Allen, H., Alsbarocks, S., Amin, A., Angulano, D., Angalebochi, V., Aogal, A., Ayodeji, M., Baca, E., Baden, H., Baladen, D., Bandaranake, D., Barber, M., Barnsted, M., Benahmed, F., Biswalo, K., Blatt, J., Blankenburg, K., Blyth, P., Brown, M., Blatt, J., Blankenburg, K., Blyth, P., Brown, M., Bhay, C., Burch, P., Burrel, R. Calderon, E., Cardenas, V., Carter, K., Carderon, E., Cardenas, V., Carter, K., Carderon, E., Chen, Y., Chen, Z., Chu, J., Clardcon, S., Danas, C., Ding, Y., Dinh, H., Duya, R., Chen, Y., Chen, Y., Chen, Z., Chu, J., Charge, J., Darano, C., Ding, Y., Dinh, H., Duya, R., Chen, Y., Carleron, M., Carleron, M., Cabisi, A., Garner, T., Garza, M., Gabrago, O., Denson, S., Dunn, A., Durbin, K., Duval, B., Eaves, V., Farser, C., K., Galisi, A., Garner, T., Garza, M., Gabrago, C., Falls, M., Garza, M., Gabrago, C., Falls, M., Garisi, A., Garner, T., Garza, M., Gabrago, C., Fraser, C., K., Galisi, A., Garner, T., Garza, M., Gabrago, C., Bray, C., Hune, J., Garner, M., Gabrago, S., Haldun, S.L., Hadden, S., Haldun, S.L., Hadden, S., Haldun, S.L., Hadden, S., Haldun, S.L., Hadden, M., Hamilton, K., Marit, M., Mahla, M., Haldun, S.L., Levis, L., Li, Z., Liu, J., Liu, W., Liu, Y., Ling, H., Johnson, B., Johnson, B., Johnson, B., Johnson, B., Johnson, B., Margam, B., Marla, K., Martin, R., 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (19-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA.

Baylor Plaza, Houston, TX 77030, USA.

The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas and whole genome shotgun sequencing reads assembled using Atlas in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the serimated size. The sequence may extend beyond the ends of the clone and there may be sequence
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Rat Genome Sequencing Consortium.
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Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae,
Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               97716 CAACCACGAAAGAAAAAGAGTCCAAGTCCGCCAAGAAGAAGAAGAGCGCTCCAAGGCCAAG
                                                                                                                                                                                                                                                                                             TyrGlnGluThrLeuLysGluIleAspAspValTyrGluLysTyrLysLysGluAspAsp :::
                                                                                                                                                                                                                                                                                                                                                                                                                                             98016 TCCAACCAGAAAAACGCCTACAGCAGCATCCCAGAGAGCGTTAATCAATAGCCAAGAA
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HTG: HTGS PHASE1; HTGS DRAFT; HTGS_FULLTOP.
Rattus norvegicus (Norway rat)
Rattus norvegicus
                                                                     Length:
Matches:
Conservative:
Mismatches:
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NOTE: This is a "working draft' sequence. It currently consists of 2 contigs. The true order of the pieces is not known and their order in this sequence record is
contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature table.
                                                                                                                                                         TyrGlnGluThrLeuLysGluIleAspAspValTyrGluLysTyrLysLysGluAspAsp :::
                                                                                                                                                                                                                                                                                                                                                                                           arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 225634: contig of 225634 bp in length 225635 225734: gap of unknown length 225735 231311: contig of 5577 bp in length. Location/Qualifiers 1.231311
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                                                                               Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
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Matches:
Conservative:
Mismatches:
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|mol_type="genomic DNA"
|db_xref="taxon:10116"
|clone="CH230-210B24"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             end_sequence:BH343917"
complement(218103. .218757)
/note="clone_boundary
clone_end:Sp6
site:
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clone_end:Sp6"
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/note="clone_boundary
clone_end:T7
                                                                     ---- Genome Center
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LeuAsnGlnLysLysArgLeuGlnGlnLeuLeuGlnArgAlaLeuIleAsnSerGlnGlu 95

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Muzny, D.Marie., Metzker, M. Lee., Abramzon, S., Adams, C., Alder, J.,
Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D.,
Anyaleberdi, V., Aoyagi, A., Ayodeji, M., Baca, B., Baden, H.,
Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F.,
Biswalo, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M.,
Bryant, N., Buhay, C., Burch, P., Burrell, K., Calderon, E.,
Cardenas, V., Carter, K., Cavazos, I., Ceasar, H., Center, A.,
Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Z., Chu, J.,
Davila, M.L., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D.,
Delgado, O., Denson, S., Deramo, C., Dinh, H., Divya, K.,
Draper, H., Dugan-Rocha, S., Dunn, A., Durbin, K., Duval, B., Eaves, K.,
Egan, A., Escotto, M., Eugene, C., Evans, C.A., Falls, T., Foster, M., Ferser, C.M., Gabisi, A., Gancia, A., Garner, T., Garza, M.,
Gebregeorgis, E., Geer, K., Gill, R., Grady, M., Guerra, W., Guevara, W.,
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53177
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Rattus norvegicus clone CH230-129P3, WORKING DRAFT SEQUENCE, 3
unordered pieces.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                               53116 AGACAAATGGAGCTGCATTCAAGGTGTTTCCAGGATCCTGCTGAAAGTGAGCGGGCCTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       216 LeuCyaAsnGlnValSerTyrGlyGluMetIleGlyCysAspAsnGluGlnCysProIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           53176 TTGGGAGATGAAAAGATTCAGATTGTCACACAGATGCTGGAATTGGTGGAAAACCGAGCC
                                                                                                                                                                                                                                                                                                                                                                                                                         156 ArgThrSerGluSerArgAspLeuCysHisMetAlaAsnGlylleGluAspCysAspAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                                           196 GlnGluArgGluAlaSerProValGluPheAlaIleAgpProAsnGluProThrTyrCys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   256 ProLysCysArgGlyAspAsnGluLysThrMetAspLysSerThrGluLysThrLysLysLys
                                                           LeuGlyAspGluLys1leGln1leValThrGlnMetLeuGluLeuValGluAsnArgAla
                                                                                                                                                                           116 ArgGlnMetGluLeuHisSerGlnCysPheGlnAspProAlaGluSerGluArgAlaSer
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AC128348.3 GI:25007900
HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP
Rattus norvegicus (Norway rat)
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Gunaratne, P., Haaland, W., Hamil, C., Hamilton, C., Hamilton, K., Harvandez, Y., Havlak, P., Hawes, A., Henderson, N., Hernandez, J., Harnandez, N., Hanes, S., Hladun, S.L., Hodgson, M., Hogues, M., Houlins, B., Howelle, S., Hladun, S.L., Hodgson, M., House, J., Globid, D., Jackson, L., Jacob, L., Jang, H., Johnson, R., Marjer, Kowar, C., Kraft, C.L., Lebow, H., Lewis, L., Lui, Z., Liu, J., Liu, Y., London, P., Longacre, S., Lopez, J., Lorensuhewa, L., Loulegedd, H., Lozado, R.J., Lui, X., Ma, J., Mahana, L., Mahindartne, M., Mahmoud, M., Malloy, K., Mangum, A., Mahana, S., McLeod, R., Martin, R., Martinez, E., Mangum, P., Martin, R., Martinez, E., Mandun, B., Mapua, P., Martin, R., Martinez, E., Mandun, B., Mapua, P., Martin, R., Martinez, E., Mandun, P., Morris, K., Morris, S., Munidasa, M., Murphy, M., Nair, L., Nandervis, C., Neal, D., Newton, N., Norris, S., Peul, H., Perez, A., Perez, L., Pfannech, C., Okwuou, G., Olarnpunsagoon, A., Pal, S., Parks, K., Paul, H., Perez, A., Perez, L., Pfannech, C., Neally, M., Ren, Y., Reuter, M., Raides, M., Raige, F., Rives, C., Paul, H., Perez, A., Rese, M., Rose, R., Raige, F., Rives, C., Rodkey, T., Rojas, A., Rose, M., Rose, R., Ruiz, S. J., Sneed, A., Sodergren, E., Sorelle, R., Sodergren, E., Sotton, A., Tabor, P., Taylor, C. Taylor, T. Thomas, N., Thomas, S., Tingey, A., Trabor, P., Taylor, T. Taylor, T. Thomas, S., Warren, R., Waigh, N., Wangh, N., Walker, B., Wang, J., Wangh, N., Walker, B., Wang, J., Walker, B., Wang, C., Wallson, R., Walker, B., Wang, J., Walght, D., Walght, R., Wullson, R., Walker, B., Wang, J., Yon, W., Walght, D., Walght, R., Wullson, R., Walder, R., Walker, Sand, R., Walles, R., Walght, D., Walder, R., Walder, R
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The sequence in this assembly is a combination of BAC based reads and Whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome
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Direct Submission
Submitted (19-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
3 (Dases 1 to 245104)
Rat Genome Sequencing Consortium.
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------ Summary Statistics
Assembly program: Phrap; version 0.990329
Consenus quality: 202567 bases at least Q40
Consenus quality: 204753 bases at least Q20
Consensus quality: 205914 bases at least Q20
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Contact: hgsc-help@bcm.tmc.edu
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AUTHORS
TITLE
JOURNAL
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JOURNAL
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COMMENT

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110957 AGACAAATGGAGCCATTCACAGTGTTCCAGGATCCTGCTGAAAGTGAGCGGCCTCA 110898
                                                                           (see http://www.hgsc.bcm.tmc.edu/docs/Genbank draft data.html). NOTE: This is a 'working draft' sequence. It currently consists of 3 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 95
Estimated insert size: 206745; sum-of-contigs estimation Quality coverage: 8x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       111077 TCAAACCAGAAAAAACGCCTACAGCAGCATCTCCAGAGAGCATTAATCAATAGCCAAGAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           56 TyrGlnGluThrLeuLysGluIleAspAspValTyrGluLysTyrLysLysGluAspAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 76 LeuAsnGlnLysLysArgLeuGlnGlnLeuLeuGlnArgAlaLeuIleAsnSerGlnGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   96 LeuGlyAspGluLysIleGlnIleValThrGlnMetLeuGluLeuValGluAsnArgAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                116 ArgGlnMetGluLeuHisSerGlnCysPheGlnAspProAlaGluSerGluArgAlaSer
                                                              NOTE: Estimated insert size may differ from sequence length
                                                                                                                                                                                                                                                                 241682: contig of 241682 bp in length 241782: gap of unknown length 242944: contig of 1162 bp in length 243044; gap of unknown length 245104: contig of 2060 bp in length.
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45075 c 46272 g 57482 t 38750 others
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/organism="Rattus norvegicus"
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clone_end:Sp6"
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240971. .241683
/note="clone_boundary
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and is derived by analysis of the total score distribution ALIGNMENTS SUMMARIES AAA53790 AAH28480 ABA09175 AAD46127 AAZ08595 standard; cDNA; 840 BP ü DB Length 1365 1108 958 1300 693 1705 1082 1772 1781 1465 8487 611 1611 987 2061 Query Match 1 49.2 49.2 49. 49. 424.5 853.5 853.5 853.5 745 AAZ08595 ט ט FAXSXWWXEX COMMand line parameters:

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| SIDSI/gcgdata/geneseq/geneseqn-embl/NA1996.DAT:* MLGQQQQQLYSSAALLTGER.....DNEKTMDKSTEKTKKDRRSR 280 5.1.6 Compugen Ltd. - nucleic search, using frame_plus_p2n model hits satisfying chosen parameters: 2552756 segs, 1349719017 residues GenCore version (c) 1993 - 2004 Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Xgapext Ygapext Fgapext Delext Minimum DB seq length: 0 Maximum DB seq length: 200000000 US-09-513-365A-1 1481 Xgapop 10.0 , X Ygapop 10.0 , Y Fgapop 6.0 , F Delop 6.0 , D Copyright

Oligonucleotide fo Human polynucleoti Human CGDD cDNA 72 Drosophila melanog

p33 tumour suppres cDNA encoding a hu

Human tumour suppr Human polynucleoti Drosophila melanog Cell cycle protein Cell cycle protein

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14

Human, TSC403; ING1L; diagnosis; lung cancer; cell cycle; regulation; cell proliferation; cell aging; apoptosis; tumour suppressor; ss.

18-OCT-1999 (first entry) Human ING1L encoding cDNA

Location/Qualifiers 1..840 Homo sapiens Key

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                                                                                            161 ArgAspLeuCysHisMetAlaAsnGlyIleGluAspCysAspAspGlnProProLysGlu
                HisSerGlnCysPheGlnAspProAlaGluSerGluArgAlaSerAspLysAlaLysMet
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P-PSDB; AAY29606.
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                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence represents the human tumour suppressor gene INGIL. The present invention also describes the human gene TSC403 expressed specifically in normal lung tissue. TSC403 is useful in the diagnosis, investigation and treatment of cancers in which it is overexpressed, including cancer of the lung, breast, fallopian tube, oesophagus, colon, thyroid, parotid gland, bladder, ovary or pancreas. INGIL is useful in the investigation of cell proliferation, aging and apoptosis and the pathology of cancer, the diagnosis and treatment of cancer such as cancer of the colon, stomach, oesophagus or fallopian tube, and the screening of candidate drugs for the treatment of such
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MetLeuGlyGlnGlnGlnGlnGnLeuTyrSerSerAlaAlaLeuLeuThrGlyGluArg
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                                                                                                                                                                                                                                                                                                                                                                                   Claim 14; Page 91; 99pp; Japanese.
                                                                                                                                                                                                                                                         Ozaki K,
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98JP-0038133.
98JP-0073234.
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                                                                                                                                                                                                                                                         Horie M, Nagata M,
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P-PSDB; AAY29606.
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                                                                WO9940190-A1
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Pred. No.:
                                                                                                                             02-FEB-1999;
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03-FEB-1998;
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The present sequence is a DNA encoding tumour suppressor homologue protein, p331NG2 which is homologous to human tumour suppressor protein, p471NG3. The tumour suppressors of the invention are involved in the regulation of cell proliferation and in the control of cellular aging, anchorage dependence and apoptosis. The tumour suppressor protein, anchorage dependence and apoptosis. The tumour suppressor protein, p471NG3, nucleic acids encoding it and antibodies against it are useful for diagnosis, prevention and treatment of tumours and cancers. The p471NG3 DNA is also used in gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tumour suppressor; p471NG3; cell proliferation; cellular aging; p331NG2; anchorage dependence; apoptosis; tumour; cancer; gene therapy; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Tumour suppressor homologue protein, p33ING2"
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                                                                                                                        AspAsnGluLysThrMetAspLysSerThrGluLysThrLysLysAspArgArgSerArg
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                                        The present sequence represents the human tumour suppressor gene INGIL. The present invention also describes the human gene TSC403 expressed specifically in normal lung tissue. TSC403 is useful in the diagnosis, investigation and treatment of cancers in which it is overexpressed, including cancer of the lung, breast, fallopian tube, ossophagus, colon, thyroid, parotid gland, bladder, ovary or pancreas. INGIL is useful in the investigation of cell proliferation, aging and apoptosis and the pathology of cancer, the diagnosis and treatment of cancer such as cancer of the colon, stomach, ossophagus or fallopian tube, and the screening of candidate drugs for the treatment of such
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SerArgLeuLeuThrCysTyrValGlnAspTyrLeuGluCysValGluSerLeuProHis
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Claim 15; Page 91-93; 99pp; Japanese.
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This sequence encodes the human tumour suppressor (TUSUP) protein. The TUSUP sequence was identified from a human lung cDNA library. The protein is 240 amino acids in length and has one potential cAMP and cGMP dependent protein kinase phosphorylation sites, into potential protein kinase phosphorylation sites, and one potential tyrosine kinase phosphorylation sites, and one potential tyrosine kinase phosphorylation sites, and one potential tyrosine kinase phosphorylation sites. TUSUP has structural and chemical similarity to p33. TUSUP can be used to treat or prevent cancer, particularly of the reproductive or gastrointestinal tracts or of the immune system. Agonists of the TUSUP protein can be used to raise TUSUP specific antibodies and to screen for specific binding agents and potential therapeutic agents. The TUSUP nucleotide sequence can be used in gene therapy and as a source of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CGGTGATGTTTCCAACCTCTTTCCCAGTCAATGGATCAGGACGGCGATCAGCAGCTCGGA 306
                                                                                                                                                                                                  New human tumour suppressor protein for treating cancer, particularly of reproductive and gastrointestinal tracts or immune system -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             69 AC-CGGCTGCTCACCTACGTGCAGGACTACCTTGAGTGCGTGGAGTCGCTGCCCCAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                               BP; 367 A; 215 C; 285 G; 265 T; 21 other;
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Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                     diagnostic probes and primers
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1345.00
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                                                             99WO-US11136
                                                                                     98US-0086359
                                                                                                              (INCY-) INCYTE PHARM INC.
                                                                                                                                       Corley NC,
                                                                                                                                                             WPI; 2000-062711/05.
P-PSDB; AAY52199.
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Best Local Similarity:
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                                                                                      28-MAY-1998;
                                                            20-MAY-1999;
             W09961612-A1
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                                                                          GACATGCAGAGGAACGTGTCTGTGCTGCGAGAGCTGGACAACAAAAATATCAAGAAACGTTA
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                                                             AspMetGlnArgAsnValSerValLeuArgGluLeuAspAsnLysTyrGlnGluThrLeu
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/product= TUSUP
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SOF ACCGICGCGGATCCTGGCTCCGCAAACGTTAAAGGAAATTGATGATGATCTTACGAAAAATA 366
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AspMetGlnArgAsnValSerValLeuArgGluLeuAspAsnLysTyrGln--
                                                                                                                                                                                     285 G; 265 T; 21 other;
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   associated disorders
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GluGlnCysProlleGluTrpPheHisPheSerCysValSerLeuThrTyrLysProLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GAACAGTGTCCAATTGAATGGTTTCACTTTTCATGTGTTTCACTTACCTATAAACCAAAG
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                             IleAsnSerGlnGluLeuGlyAspGluLysIleGlnIleValThrGlnMetLeuGluLeu
                                                                ATTAATAGTCAAGAATTGGGAGATGAAAAATACAGATTGTTACACAAATGCTCGAATTG
                                                                                               ValGluAsnArgAlaArgGlnMetGluLeuHisSerGlnCysPheGlnAspProAlaGlu
                                                                                                                                                                 SerGluArgAlaSerAspLysAlaLysMetAspSerSerGlnProGluArgSerArg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gene;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Detecting nucleic acid encoding exon 1b of ing1, useful for diagnosing and treating cancer, comprises contacting sample with isolated nucleic acid comprising sequence of exon 1b and detecting hybridized products
ACGCTCCAAGGCAAGCAGGAAAGGAAGCTTCACCTGTTGAGTTTGCAATAGATCCTAA
                                  nGluProThrTyrCysLeuCysAsnGlnValSerTyrGlyGluMetIleGlyCysAspAs
                                                    787 TGAACCTACATACTGCTTATGCAACCAAGTCTCTTATGGGGAGATGATAGGATGTGGACAA
                                                                                                                        TGAACAGTGTCCAATTGAATGGTTTCACTTTTCATGTGTTTCACTTACCTATAAACCAAA
                                                                                                                                                                      sGlyLysTrpTyrCysProLysCysArgGlyAspAsnGluLysThrMetAspLysSerTh
                                                                                                                                                                                                        GGGGAAATGGTATTGCCCAAAGTGCAGGGGGATAATGAGAAAAAAATGGACAAAAGTAC
                                                                                                  nGluGlnCysProlleGluTrpPheHisPheSerCysValSerLeuThrTyrLysProLy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    p53; tumour; cancer; detection; antibody; hybridisation; exon 1b; ING1; ing1; p331NG1; p371NG1; oncogene; gene therapy; diagnosis; proliferation disorder; transformation; transformed cell; mouse; ds.
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/product= P37ING1 polypeptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Murine P37ING1 coding sequence.
                                                                                                                                                                                                                                                                                                                                                 AAA53790 standard; cDNA; 2817
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Expression of one promoter have been discovered.

Expression of one promoter (la) produces a protein identical to ING1. Expression of a second promoter (lb) produces a protein having an identical C-terminal fragment to ING1 but an additional 104 or terminal amino acids. The newly discovered protein has been designated p371NG1 (Wild type: p31NG1). p371NG1 has the characteristics of an oncogene. When overexpressed in cells (even those expressing wild type p53) p371NG1 is able to cause to proliferation or transformation of those cells. Thus detecting a nucleic acid encoding exon 1b of ing1 by hybridisation with an isolated nucleic acid having the sequence of exon 1b of ing1 or its antisense sequence can identify individuals expressing the concegenic form of ing1. Novel peptide sequences taken from the 104 or terminal peptide of p371NG1 can also be used to raise antibodies that can also be used in detection methods for treatment of cell proliferation disorders, especially cancers and for diagnosing and
exons of the ing
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Sequence 2817 BP; 670 A; 711 C; 846 G; 590 T; 0 other;

Alignment Scores: Pred. No.: Score: Percent Similarity: Best Local Similarity: Query Match:	5.46e-74 874.50 77.41% 61.11% 59.05%	Length: Matches: Conservative: Mismatches: Indels:	2817 165 50 11
US-09-513-365A-1 (1-280) x AAA53790 (1-2817)) x AAA53790	(1-2817)	
Oy 18 GlyGluArg	1SerArgieuleuT	hrCysTyrValGlnAsp	18 GlyGluArgSerArgLeuLeuThrCysTyrValGlnAspTyrLeuGluCysValGluSer

		GlyGluArgSerArgLeuLeuThrCysTyrValGlnAspTyrLeuGluCysValGluSer 37 ::: GGGGAGCAGATCCACCTGGTGAACTATGTGGAGATTACCTGGACTCAATCGAGTCA 921	LeuproHisaspMetGlnArgasnValSerValLeuArgGlubeuAspAsnLysfyrGln 57 	GluThrLeulysGlu1leAspAspValTyrGluLysTyrLysLysBysGluAspAspLeuAsn 77	GInLysLysArgLeuGlnGlnLeuLeuGlnArgAlaLeulleAsnSerGlnGluLeuGly 97	AspGluLysIleGlnIleValThrGlnMetLeuGluLeuValGluAsnArgAlaArgGln 117 	MetGluLeuHisSerGlnCysPheGlnAspProAlaGluSerGluArgAla 134	SerasplysalalysmethspSerSerGlnProGluarg	SerSerargargProargArgGlnargThrSerGluSerargaspLeuCysHisMetAla 167 :::::: ::: ::: AataacaaGGGTCCAGGAGGCAGCAAACAATGAGAATCGAGAGAAGGGGTCGAATAAT 1341	AsnGlyIleGluAspCysAspAspGlnProProLysGluLysLysSerLysSerAlaLys 187 :::	LystystysBargSertysAlatysGlnGluArgGluAlaSerProValGluPheAlaIle 207
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             diagnosing
                                                                                                                                                                                   LysProLysGlyLysTrpTyrCysProLysCysArgGlyAspAsnGluLysThrMetAsp
                                                                                                                                                                                                              Detecting nucleic acid encoding exon 1b of ing1, useful for diagnosing and treating cancer, comprises contacting sample with isolated nucleic acid comprising sequence of exon 1b and detecting hybridized products
                                                                             CysAspAsnGluGlnCysProlleGluTrpPheHisPheSerCysValSerLeuThrTyr
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Expression of one promoter (1a) produces a protein identical to ING1. Expression of a second promoter (1b) produces a protein havin an identical C-terminal targement to ING1 but an additional 104 N-terminal amino acids. The newly discovered protein has been designated p37ING1 (Wild type: p33ING1). p37ING1 has the characteristics of an oncogene. When overexpressed in cells (even
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         p53; tumour; cancer; detection; antibody; hybridisation; exon 1b;
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63 GGGGAGCACCACCAGGAGAAC---TATGTGGAGGACTACCTGGACTCCATCGAGTCC 119
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those expressing wild type p53) p371NG1 is able to cause proliferation or transformation of those cells. Thus detecting a nucleic acid encoding exon 1b of ing1 by hybridisation with an isolated nucleic acid having the sequence of exon 1b of ing1 or its antisense sequence can identify individuals expressing the oncogenic form of ing1. Novel peptide sequences taken from the 104 N-terminal peptide of p371NG1 can also be used to raise antibodies that can also be used in detection methods for the p371NG1 variant. The polypeptides may be useful in gene therapy for treatment of cell proliferation disorders, especially cancers and for diagnosing and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     118 MetGluLeuHisSerGlnCysPheGlnAspProAlaGlu-----
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826 AGCGGCAAGGCTGGCGGGACAGGCCCAAAGGCGAGGGGGCAGCGCAGGCTGACAAGGCCC 885
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                                                                                                                                                                                                                                                                                               118 MetGluLeuHisSerGlnCysPheGlnAspProAlaGlu---SerGluArgAlaSerAsp 136
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; gene; ss; monoclonal antibody; epitope; inhibitor of growth 1; ING1; tumour suppressor; cell cycle; breast tumour; lymphoid malignancy; cell growth; anti-ING1; CAb; isoform; diagnosis; tumour; antigen; p331NG1b.
                                                  646 CAGAAGCGGGGATGCTGCACTGTGTGCAGCGCGCTGATCCGCAGCCAGGAGCTGGCG
                                                                                                                                                                                                                                               AspGluLysIleGlnIleValThrGlnMetLeuGluLeuValGluAsnArgAlaArgGln
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                                      GlyGluArgSerArgLeuLeuThrCysTyrValGlnAspTyrLeuGluCysValGluSer
                                                                                                                                                                                            GlnLysLysArgLeuGlnGlnLeuLeuGlnArgAlaLeuIleAsnSerGlnGluLeuGly
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            268 LysSerThrGluLysThrLysLysAspArg 277
              US-09-513-365A-1 (1-280) x AAH28478 (1-1533)
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               833
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The sequence is a variant of the ING1 gene, which is a tumour suppressor gene candidate. The cancer associated antigen polynucleotides and polypeptides are useful for screening for the possible presence of a pathological condition in a subject such as cancer. The cancer associated antigen polypeptides are useful for producing vaccines.
                                                                                                                                                                                                                      Cancer associated antigen; ING1; tumour suppressor; cancer; vaccine; ss.
             774 AATCATAAACCCAAGGGCAAGTGGTACTGTCCCAAGTGCCGGGGGGAGAACGAGAACC
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Isolated cancer associated nucleic acid molecule identified by SEREX (serological identification of antigens by recombinant expression cloning) technique, useful in nucleic acid based therapies to treat
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                                                                                                                                                                                            Nucleotide sequence of a human cancer associated antigen.
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(SLOK ) SLOAN KETTERING INST CANCER RES.
(CORR ) CORNELL RES FOUND INC.
                                                                                                                                                                                                                                                                       Location/Qualifiers
451..1290
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                                                                                                                   DNA; 1533
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853.50
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24-OCT-2000; 2000US-0602362.
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                                                                                                                  AAH28478 standard;
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GluThrieulysGluIleAspAspValTyrGluLysTyrLysLysGluAspAspLeuAsn 77
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                                                                                                                                                                                                                                                                                                                                                                                                            The invention discloses monoclonal antibodies which can be used, in combination, to specifically recognise epitopes of ING1 (inhibitor of growth 1) protein isoforms. ING1 is a tumour suppressor gene and its expression is regulated through the cell cycle, peaking in the S phase. Expression of ING1 is down regulated in breast tumours and lymphoid malignancies. Overexpression of a construct containing the ING1 gene is able to inhibit cell growth by reducing the fraction of cells which enter into the S phase. The monoclonal antibodies are useful for detecting an corredgenously expresses ING1 protein. The anti-ING1 monoclonal antibody combination consists of two or more antibodies of CAbl-CAbl0 (not defined), preferably amxure of CAbl-CAbs, which can detect at least two different isoforms of ING1. The antibodies are also useful for diagnosing a disease e.g. tumour or medical condition in an animal (preferably, human) associated with aberrant levels of an ING1 protein. The sequence presented is the human inhibitor of growth 1 (ING1) isoform, or more insease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LeuProHisAspMetGlnArgAsnValSerValLeuArgGluLeuAspAsnLysTyrGln 57
                                                                                                                                                                                                                                                                                                                               Novel monoclonal antibody which specifically recognizes epitope of ING1, inhibitor of growth 1 protein, and designated CAb1-10, useful for detecting two different isoforms of ING1 and diagnosing a medical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18 GlyGluArgSerArgLeuLeuThrCysTyrValGlnAspTyrLeuGluCysValGluSer
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                                                                   /product= "p33ING1b"
                                 Location/Qualifiers
873..1712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein used to raise antibodies.
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26-FEB-1999; 99US-0258372.
15-NOV-1996; 96US-0751230.
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22-MAR-2000; 2000US-0532868
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Best Local Similarit
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(BOLA/) |
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1428 AAGAAGAGGCTCCAAGGCCAAGGCGGAGGAGGGGTCCCCTGCCGACCTCCCCATC 1487
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                                                                                                                                                                    98 AspGluLysIleGlnIleValThrGlnMetLeuGluLeuValGluAsnArgAlaArgGln 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AspProAsnGluProThrTyrCysLeuCysAsnGlnValSerTyrGlyGluMetIleGly 227
                                                                                                                                                                                                                                                                               118 MetGluLeuHisSerGlnCysPheGlnAspProAlaGlu---SerGluArgAlaSerAsp 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    148 SerSerArgArgProArgArgGlnArgThrSerGluSerArgAspLeuCysHisMetAla 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CysAspAsnGluGlnCysProIleGluTrpPheHisPheSerCysValSerLeuThrTyr 247
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                248 LysProLysGlyLysTrpTyrCysProLysCysArgGlyAspAsnGluLysThrMetAsp
                                                                     GlnLysLysArgLeuGlnGlnLeuLeuGlnArgAlaLeuIleAsnSerGlnGluLeuGly
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1668 AAAGCCCTGGAGAAATCCAAAAAAGAGAGG 1697
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                                                                                                                                                                                                                                                                                                                                                                                 137 LysAlaLysMetAspSerSerGlnPro---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAA53789 standard; cDNA; 1835 BP
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human tumours and tumour cell lines, but functional inactivation of the p53 gate burner tumours and tumour cell lines, but functional inactivation of the p53 gate the p53 gathway occurs in a much larger proportion of the p53 gate and y cases the mechanism of functional inactivation of the p53 gate remains unknown but p53 has been found to act in cooperation with ING1. Functional cooperation between ING1 and p53 suggested that ING1 plant p53 suggested that is ING1 encoded a tumour suppressor protein that functioned within the p53 pathway. This data suggested a possible role for ING1 in head and neck cancers and chromosomal location of the ING1 placed it vertain a region that is frequently rearranged in head and neck cancers undations in ING1 nor significant variations in its requently that ING1 was not a useful gene to study in cancer etiology. However, alternative initiation exons of the ing1 gene, each having their own promoter lave been discovered.

Expression of one promoter (1a) produces a protein having an identical C-terminal fragment to ING1 but an additional 104 of ING1. Expression of a second promoter (1b) produces a protein has been can identifical C-terminal fragment to ING1 but an additional 104 of Lose expressing wild type ing1) by the protein has the class of an oncogene. When overexpressed in cells (even those expressing wild type p53) p371NG1 is able to cause proliferation or transformation of those cells. Thus detecting a nucleic acid encoding exon 1b of ing1 by thypridisation with an ancoding exon 1b of ing1 by thypridisation with an oncogene. When overexpressed in cells of ing1 novel peptide sequences taken from the log concerning form of ing1 novel peptide sequences a protein detecting a the terminal peptide of p371NG1 can also be used in detection methods for the p371NG1 variant. The polypeptides may be useful in gene theres and encoded concer
                                                                                                                                                              Detecting nucleic acid encoding exon 1b of ing1, useful for diagnosing and treating cancer, comprises contacting sample with isolated nucleic acid comprising sequence of exon 1b and detecting hybridized products
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               eration disorders, especially cancers and for diagnosing and
                                                       Grigorian IA;
                                                       Gurova KV,
                                                                                                                                                                                                                                                                                 Claim 17; Fig 6; 134pp; English.
(UNII ) UNIV ILLINOIS FOUND.
                                                    Zeremski M,
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Sequence 1835 BP; 541 A; 387 C; 468 G; 439 T; 0 other; 1835 140 35 43 10 Conservative: Mismatches: Matches: Length: Indels: Gaps: 8.55e-62 745.00 76.75% 61.40% 50.30% Percent Similarity: Best Local Similarity: Alignment Scores: Query Match:

CGCCGGGTACTGCACTGCATCCAGAGGCCCTGATCCGCAGCCAGGAGCTAGGCGATGAG 125 LysileGlnIleValThrGlnMetLeuGluLeuValGluAsnArgAlaArgGlnMetGlu 119 136 79 65 66 LeuHisSerGlnCysPhe-----GlnAspProAlaGluSerGluArgAlaSerAsp LeutysGlulleAspAspValTyrGluLysTyrLystysGluAspAspLeuAsnGlnLys LysArgLeuGlnLeuLeuGlnArgAlaLeuIleAsnSerGlnGluLeuGlyAspGlu US-09-513-365A-1 (1-280) x AAA53789 (1-1835) 9 80 99 001 126 120 186

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306 AAGCGGTCCAGGAGGCAGCGAAACAATGAGAATCGAGAGAACGCGTCGAATAATCACGAC 365
                246 AAGGCGGGCCAGGACAAGTCGAAGAGTGAGGCCATCACACAGGCCAGATAAGCCGAATAAC 305
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                                                150 ArgArgProArgArgAnArgThrSerGluSerArgAspLeuCysHisMetAlaAsnGly
                                                                                                                   AsnGluProThrTyrCysLeuCysAsnGlnValSerTyrGlyGluMet11eGlyCysAsp
                                                                                                                                                                                                                                                                            LysGlyLysTrpTyrCysProLysCysArgGlyAspAsnGluLysThrMetAspLysSer
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                                                                                                                                                      LysArgSerLysAlaLysGlnGluArgGluAlaSerProValGluPheAlaIleAspPro
                                                                                                     170 IleGluAspCysAspAspGlnProProLysGluLysLysSerLysSerAlaLysLys
                                                                                                                                                                                426 AAACGCTCCAAGGCCAAAGCAGAGGGAAGCGTCTCCTGCCGACCTTCCCATCGACCCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Isolated cancer associated nucleic acid molecule identified by SEREX (serological identification of antigens by recombinant expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ala)"
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/transl except= "(pos: 124.126, aa: Pro,
/poroduct= "cancer asscociated antigen"
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(CORR ) CORNELL RES FOUND INC.
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24-OCT-2000; 2000US-0602362.
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standard; cDNA; 1902 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                              ------SerGluArgAlaSerAspLysAlaLysMetAspSerSer 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         144 GlnProGluArgSerSerArgArgProArgArgGlnArgThrSerGluSerArgAspLeu 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               164 CysHisMetAlaAsnGlyIleGluAspCysAspAspGlnProProLysGluLysLysSer 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         603
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           604 AAGACCTCCAAGAAGAAGAAGCGCTCCAAGGCCAAGGCGGAGGCGAGAGGCGTCCCCTGCC 663
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            784 GGGCTCAATCATAAACCCAAGGGCAAGTGGTACTGTCCCCAAGTGCCGGGGGGAGAACGAG 843
                                                            The present sequence encodes a human cancer associated antigen. The sequence is the wildtype of the ING1 gene, which is a tumour suppressor gene candidate. The cancer associated antigen polynucleotides and polypeptides are useful for screening for the possible presence of a pathological condition in a subject such as cancer. The cancer associated antigen polypeptides are useful for producing vaccines.
                                                                                                                                                                                                                                                                                                                                                                             95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       #30 GGCAACAGCGGAAGGTTGGCGCGGGACAGGCCCAATGGCGATGCGGTAGCGCAGTCTGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GACCTCCCCATCGACCCCAACGAACGAACTGTCTGTGTGAACCAGGTCTCCTATGGG
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cloning) technique, useful in nucleic acid based therapies to treat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                116 ArgGlnMetGluLeuHisSerGlnCysPheGlnAspProAlaGlu
                                                                                                                                                          Sequence 1143 BP; 289 A; 291 C; 366 G; 197 T; 0 other;
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Matches:
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                                     Page 44; 62pp; English.
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LeuAsnGlnLysLysArgLeuGlnGlnLeuLeuGlnArgAlaLeuIleAsnSerGlnGlu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A partial cDNA clone (AAT69651), designated ING1, codes for a novel tumour suppressor protein p331NG1 (AAW19118) that is a potent inhibitor of cell growth. It was isolated by subtractive theybridisation between normal mammary and transformed epithelial cDNAs, isolation of an antisense ING1 cDNA insert that caused increased cell proliferation, and use of the insert to screen normal human fibroblast and Hela cDNA libraries. A complete ING1 sequence (AAT69652) was obtd. by 5'RACE. ING1 is localised to the 13433-34 chromosome region, to which a number of human cancers have been mapped. ING1 nucleic acids can be used in the diagnosts of breast cancer, a decreased level of ING1 mRNA indicates cancerous cells.
                                                                                          Tumour suppressor gene; ING1; p33ING1; breast cancer; brain cancer; diagnosis; gene therapy; ss.
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08-DEC-1995;
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        LeuGlyAspGluLysIleGlnIleValThrGlnMetLeuGluLeuValGluAsnArgAla 115
                                                                                 -----SerGluArgAlaSerAspLysAlaLysMetAspSerSer 143
                                                                                                   271 GGCAACAGCGGCAAGGTTGGCGGGACAGGCCCAATGGCGATGCGGTAGCGCAGTCTGAC 330
                                                                                                                     GlnProGluArgSerSerArgArgProArgArgClnArgThrSerGluSerArgAspLeu 163
                                                                                                                                331 AAGCCC-----AACAGCAAGCGCTCACGGCGGCAGCGCAACGAGAACCGTGAGAAC 384
                                                                                                                                                         164 CysHisMetAlaAsnGlyIleGluAspCysAspAspGlnProProLysGluLysLysSer 183
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                                                                                                                                                                                                                                                                     GluMet.leGlyCysAspAsnGluGlnCysProlleGluTrpPheHisPheSerCysVal
                                                                                                                                                                                                                                                                               SerbeuThrTyrLysProLysGlyLysTrpTyrCysProLysCysArgGlyAspAsnGlu
                                                                                                                                                                                                                                                  ING1 gene; p331NG1; human; apoptosis; cell death; breast cancer;
brain tumour; gene therapy; tumour suppressor; ss.
                                                                                                                                                                                                                                                                                                                                                       LysThrMetAspLysSerThrGluLysThrLysLysAspArg 277
                                            ArgGlnMetGluLeuHisSerGlnCysPheGlnAspProAlaGlu-
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Growth) partial cDNA clone that codes form a pulling of growth partial cDNA clone that codes form a pliling polypeptide (see AAW79674), a novel inhibitor of cell growth and a candidate (see AAW79674), a novel inhibitor of cell growth and a candidate cumour suppressor. Into is a new gene that is expressed in normal mammary epithelial cells, but which is expressed in normal ceveral cancerous mammary epithelial cell lines and is one expressed in many primary brain tumours. To isolate ING1, a subtractive hybridisation of brasat cancer cell line cDNAs was performed with CDNA from normal mammary epithelial cells, and subtracted cDNAs were cloned into retrovirus vector pLNCX. Following passage through a packaging line, normal mouse mammary epithelial cells were infected, and infected cells were infected into nude mice. Putative transforming fragments from tumours were isolated by PCR (see AAV62299-1) and subcloned into LNCX. An ING1 fragment was obtained and used to screen normal human fibroblast and Heia cell cDNA libraries. 2 clones were sequence (see AAV6229) was obtained by RACE. A claimed method to botain the partial ING1 sequence. The complete cDNA sequence (see D33ING1 peptide or an oligonucleotide encoding such as a peptide. AAV6229) was obtained for inhibiting apoptosis in a eukaryotic cell involves administering an antisense oligonucleotide. Also claimed are a method for determining the apoptotic characteristics of a claimed are method for inhibiting apoptosis in a eukaryotic cell, an assay for determining the level of p33ING1 ectivity in a eukaryotic cell, and an isolated eukaryotic cell, an else vector and an isolated eukaryotic cell, and an else sequence and an else sequence and else solations and an isolated eukaryotic cell, an else sequence and else sequence and else solations and else solations and else sola
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Modulating eukaryotic apoptosis by increasing p331NG1 activity -using p331NG1 derivatives, to induce apoptosis in cancer cells, and in the investigation of apoptotic pathways
                                                                                                                                                                                                                                                                         the nucleotide sequence of a human ING1 (INhibitor
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                                                                                                                                                                                     Example 2; Fig 2; 66pp; English.
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proventing or treating inflammation, or disorders associated with cell; proliferation and apoptosis e.g. bone cancer, brain cancer, cervix cancer, adenocarcinoma, leukaemia, lymphoma or melanoma. They are particularly useful as models for developing human therapeutic targets, identifying therapeutic proteins, or serving as targets for the development of human therapeutic agents that modulate tumour suppressor protein activity in cells and tissues that express the tumour suppressor protein activity, in cells and tissues that express the tumour suppressor protein. Polypeptides of the invention are used for identifying agents that modulate their activity. They are useful for raising antibodies or cliciting an immune response; as a reagent in assays designed to quantitatively determine levels of the protein (or its binding partner or ligand) in biological fluids; or as markers for tissues in which the corresponding protein is preferentially expressed. The invention is also used as vaccines. The present sequence is human tumour suppressor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AspGluLys1leGlnIleValThrGlnMetLeuGluLeuValGluAsnArgAlaArgGln 117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       58 GluThrLeuLysGluIleAspAspValTyrGluLysTyrLysLysGluAspAspLeuAsn 77
polynucleotides. Sequences of the invention are useful for diagnosing,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          812 GACCCCAACGAACCCACGTACTGTCTGTGCAACCAGGTCTCCTATGGGGAATGATCGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LysProLysGlyLysTrpTyrCysProLysCysArgGlyAspAsnGluLysThrMetAsp
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                                                                                                                                                                                                                                                                                                                                      528 G; 417 T; 0 other;
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         CysHisMetAlaAsnGlyIleGluAspCysAspAspGlnProProLysGluLysLysSer 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; tumour suppressor protein; cell proliferative disorder; vaccine; inflammation; brain cancer; adenocarcinoma; cervix cancer; bone cancer; apoptosis; leukaemia; lymphoma; melanoma; therapy; chromosome 13; gene;
                               GluPheAlaIleAspProAsnGluProThrTyrCysLeuCysAsnGlnValSerTyrGly :::
                                                                                                                                                                                                                          GluMetIleGlyCysAspAsnGluGlnCysProIleGluTrpPheHisPheSerCysVal
                                                                                                                                                                                                                                                SerLeuThrTyrLysProLysG1VLysTrpTyrCysProLysCysArgG1yAspAsnG1u
                                                                                                                                                                                                                                                                                                                   New human tumor suppressor proteins, useful for developing human therapeutic agents, or preventing or treating inflammation, or disorders associated with cell proliferation, e.g. bone cancer, brain
                                                                                LysSerAlaLysLysLysArgSerLysAlaLysGlnGluArgGluAlaSerProval
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/product= "Human tumour suppressor protein"
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                                                                                                                                                                                                                                                                                                                                                                                        Human tumour suppressor protein encoding cDNA.
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5'UTR
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136

451

97

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A full-length cDNA clone (AAT69652), designated ING1, codes for a novel 33 kDa tumour suppressor protein p33ING1 (AAW19119), formerly c p33IG1, that is a potent inhibitor of cell growth. A partial clone (AAT69651) was isolated by subtractive hybridisation between normal mammary and transformed epithelial cDNAs, isolation of an antisense ING1 cDNA insert that caused increased cell proliferation, and use of the insert to screen normal human fibroblast and HeLa cDNA libraries. The complete ING1 sequence was then obtd. by 5'RACE. ING1 is localised to the 13q33-34 chromosome region, to which a c number of human cancers have been mapped. ING1 nucleic acids can be used in the diagnosis of breast cancer; a decreased level of ING1 mRNA indicates cancerous cells. They can also be used in gene therapy methods to block the proliferation of cancer cells.
                                                                                                                                                                                          Tumour suppressor gene; ING1; p33ING1; breast cancer; brain cancer; diagnosis; gene therapy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Isolated tumour suppressor gene, ING1 - useful to develop products for inhibiting or increasing cell proliferation, in particular for treatment or diagnosis of cancer
                                                                                                                                                                  Tumour suppressor gene ING1 full-length cDNA
              992 AAAGCCCTGGAGAAATCCAAAAAAGAGAGG 1021
268 LysSerThrGluLysThrLysLysAspArg 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                       /*tag= e
/note= "reverse primer 4"
                                                                                                                                                                                                                                                                                                                                                                                                             *tag= d
note= "reverse primer 3"
                                                                                                                                                                                                                                                                                                                                                                    /*tag= c
/note= "direct primer 2"
857..876
                                                                                                                                                                                                                                                                                                                                           <u>-</u>
                                                                                                                                                                                                                                                                                                                          /*tag= b
/note= "direct primer
complement (763..782)
                                                                                                                                                                                                                                                                                                             complement (474..494)
                                                                                                                                                                                                                                                                   Location/Qualifiers
16..900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TECHNOLOGIES INT INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 11; Fig 3; 63pp; English.
                                                                               AAT69652 standard; cDNA; 2061
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                96US-0751230.
95US-0569721.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      96WO-CA00819
                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Garkavstev I, Riabowol K;
                                                                                                                                                                                                                                                                                                                                                                                                                                         890..900
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P-PSDB; AAW18119.
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                                                                                                                                                                                                                                         Homo sapiens
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08-DEC-1995;
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LeuGlyAspGluLysIleGlnIleValThrGlnMetLeuGluLeuValGluAsnArgAla 115
                                                                                                                                                                                                                                           369
                                                                                                                                             249
                                                                                                                                                                                                                                                                                 ------SerGluArgAlaSerAspLysAlaLysMetAspSerSer 143
                                                                                                                                                                                                                                                                                                                                  144 GInProGluArgSerSerArgArgProArgArgGlnArgThrSerGluSerArgAspLeu 163
                                                                                                                                                                                                                                                                                                                                                                                          490 AAGĆĆC-----AACAGCAAGĆGCTCAČGGČGGCAĞCGCAACAACGAGAACĞTGAGAAC 543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                223
                                                                                                                                                                                                                                                                                                                                                                                                                  164 CysHisMetAlaAsnGlyIleGluAspCysAspAspGlnProProLysGluLysLysSer 183
                                                                                                                                                                                                                                                                                                                                                                                                                                   LysSerAlalysLysLysLysArgSerLysAlaLysGlnGluArgGluAlaSerProVal 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            723
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               244 SerLeuThrTyrLysProLysGlyLysTrpTyrCysProLysCysArgGlyAspAsnGlu 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             95
                                                                                                                                                                                  310 CTGGGCGACGAGAAGATCCAGATCGTGAGCCAGATGGTGGAGCTGGTGGAGAACCGCACG
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664 GACCTCCCCATCGACCCCAACGAACCCAGTACTGTCTGTGCAACCAGGTCTCTATGGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             76 LeuAsnGlnLysLysArgLeuGlnGlnLeuLeuGlnArgAlaLeuIleAsnSerGlnGlu
                                                                                                                                                                                                                                                                   116 ArgGlnMetGluLeuHisSerGlnCysPheGlnAspProAlaGlu-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GluPheAlaIleAspProAsnGluProThrTyrCysLeuCysAsnGlnValSerTyrGly
                                                                                                                     56 TyrGlnGluThrieuLysGluIleAspAspValTyrGluLysTyrLysLysGluAspAsp
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          2061
136
39
45
14
          Length:
Matches:
Conservative:
Mismatches:
                                                          Indels:
                                                                                             US-09-513-365A-1 (1-280) x AAT69652 (1-2061)
        4.28e-60
728.00
74.79%
58.12%
49.16%
                                  Percent Similarity:
Best Local Similarity:
Alignment Scores:
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Search completed: January 12, 2004, 19:43:20 Job time : 276 secs

Sequence 2061 BP; 602 A; 439 C; 515 G; 505 T; 0 other;

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AKO48800

Mus musculus O day neonate cerebellum cDNA, RIKEN full-length enriched library, clone:C230071A14 product:inhibitor of growth family, member 1-like, full insert sequence.

AKO48800

AKO48800.1 GI:26339579

HTC; CAP trapper.

Mus musculus (house mouse)

Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                       BE796780 60119125
BI54854 601191255
BU258674 603104254
BU386788 603581891
BU331498 603489003
BU53199 AGENCOURT
BU51940 01.E.EJI-
BU61390 U.E.EJI-
BU61390 U.E.EJI-
BU61390 U.E.EJI-
BU196949 AGENCOURT
BU900292 AGENCOURT
BU900292 AGENCOURT
BU9001947 60258535
BE114684 7566608.x
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BU226578 603796130
AL673816 AL673816
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BE839460 RC3-FN014
BP110430 BP110430
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BE831862 RC6-MT006
AL874284 AL874284
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BG211544 RST31111
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CA982474 AGENCOURT
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BI495873 df121d04.
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BI546850 603189754
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AI885642 wl59h01.x
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                              Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                  AK048800 Mus
AK083144 Mus
                                                                                                                                                       Description
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BG211544
BE796780
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BF114684
AV647917
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BIS46850
AA204672
AI885642
BU264721
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BU404104
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BP110430
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CA982474
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Match Length DB
gb_gss2:*
29:
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933.5
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1027
1024
1022
1007.5
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965
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897
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AK048800
LOCUS
DEFINITION
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VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                   Result
No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -MODEL-frame+ p20.model -DEV=xlp
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-Q=/Cgn2 1/USPTO spool p/US09513365/runat_12012004_163932_28778/app_query.fasta_1.455
-DB=EST _OFWT=fastap = VGUFFIX=P2D1.rst -MINIATE=0.1 -LOOPCI=0 -LOOPEX=0
-UNITS=bits -STRAT=1 -END=-1 -MATRIX=blosum62 -TRAN=buman40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MINISO -ALIGN=15 -MODE=LOCAL
-OUTFWT=pto -NORM=ext -HEAPSIZE=500 -MINIENS=0 -MAXIENS=200000000
-USER=US09513365_@CGN 1 13-549_@runat_12012004_163932_28778 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG SCORES=0 -MAIT -DSPBLCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
                                                                                                             January 12, 2004, 19:38:43; Search time 2031 Seconds (without alignments) 3350.691 Million cell updates/sec
                                                                                                                                                                                                                      MLGQQQQQLYSSAALLTGER.....DNEKTMDKSTEKTKKDRRSR 280
              GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                             - nucleic search, using frame_plus_p2n model
                                                                                                                                                                                                                                                                                                                                                             22781392 seqs, 12152238056 residues
                                                                                                                                                                                                                                                                                                                                                                                          Total number of hits satisfying chosen parameters:
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Xgapop 10.0 , Xgapext
Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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Maximum DB seq length: 2000000000
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em_gss_rod:*
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em_gss_vrl:*
gb_gssl:*
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Perfect score:
                                                                                                                                                                                                                                                        Scoring table:
                                                                               OM protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Database :
                                                                                                                                                                                                                        Sequence:
                                                                                                                                                                                                                                                                                                                                                             Searched:
                                                                                                                 Run on:
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|protein_id="Baz3461.1"
|db_xref="GI:68339880"
|translation="MLGQQQQQLYSSAALLTGERSRLLSCYVQDYLECVESLPHDMQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RNVSVLRELDNKYQETLÄETÖDYTEKYKKEDDSNQKKRLQQHLQRALINSQELGDEKT
QTOQALETVURNARQWELHSQCKOPDAESBRASDKSKWDSSQPERSSERPRRQRTSE
SIDLCHMTNOT IDDODPOPPERRASKSAKKKKSKAKQERES PVEFALDPNEFTYCLC
NQVSYGEMIGCDNEQCPIEWPHFSCVSLTYKPKGKWYCPKCRGDNEKTMDKSTEKTKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /tissue type="cerebellum"
/clone lib="RIKEN full-length enriched mouse cDNA library"
/dev stage="0 day neonate"
476, 1321
                                Yokohama,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100 LysileGlnIleValThrGlnMetLeuGluLeuValGluAsnArgAlaArgGlnMetGlu 119
                                                                                                                                                                                   in Riken
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                                                                                                                                                cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Rike Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Exploration Research Group, RIKEN Genomic Sciences Center (GSC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 476 ATGTTAGGGCAGCAGCAGCAGCAGCAGCTGTACTTCGTCGCCGCCCCCTCTGACCGGAGAG
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                   RIKEN Yokohama Institute; 1.7-22 Suehiro-cho, Tsurumi-ku, Yol
Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,
Fax:81-45-503-9216)
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                                                                                                                                                                                                                                                                      prepare mouse tissues.
Please visit our web site for further details.
URL:http://genome.gsc.riken.go.jp/.
URL:http://fantom.gsc.riken.go.jp/.
Location/Qualifiers
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/strain="C57BL/6J"
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Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

Nature 420, 563-573 (2002)

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Adachi,J., Aizawa,K., Akimura,T., Hara,A., Hashizume,W.,
Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W.,
Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Kasukawa,T.,
Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M.,
Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M.,
Nakamura,M., Nishi,K., Nomura,Y., Kondo,S., Konno,H., Sakai,K., Sakazume,N.,
Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N.,
Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Takahashi,F., Takaku,Akahira,S.,
Takeda,Y., Tanawa,A., Takahashi,F., Takaku,Akahira,S.,
Takeda,Y., Tanaka,T., Tomaru,A., Towar,Y., Yosunishi,A.,
Direct Submission

Li Submitted (16-Jul.-2001) Yoshihide Hayashizaki, The Institute of
Physical and Chemical Research (RIKEN), Laboratory for Genome
                                                                                                                                                            Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes Genome Res. 10 (10), 1617-1630 (2000)
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Nature 409 (6821), 685-690 (2001)
                      Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999) MAM
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Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y., Arakawa, T., Hara, A., Fukunishi, Y., Konno, H., Adachi, J., Fukuda, S., Arakawa, T., Hara, A., Fukunishi, Y., Kayosawa, H., Kondo, S., Yamanaka, I., Saito, T., Osiobori, T., Bono, H., Kasukawa, T., Saito, R., Kadota, K., Matsuda, H., Ashburner, M., Batalov, S., Casavant, T., Kadota, K., Matsuda, H., Rasukawa, T., Saito, R., Kuchi, P., Lewis, S., Matsuo, Y., Nikaido, I., Pesole, G., Kochiwa, H., Kuchi, P., Lewis, S., Matsuo, Y., Nikaido, I., Pesole, G., Tomita, M., Wagner, L., Washio, T., Sakai, K., Okido, T., Furuno, M., Aono, H., Baldarelli, R., Besole, G., Blake, J., Boffelli, D., Bojunga, N., Carninci, P., de Bonaldo, M., Brownstein, M.J., Bult, C., Fletcher, C., Fujita, M., Gariboldi, M., Gustincich, S., Hill, D., Hofmann, M., Hume, D.A., Kamiya, M., Lee, N.H., Lyons, P., Nordone, P., Ring, B., Ringwald, M., Rodriguez, I., Sakamoto, N., Sasaki, H., Toyo-oka, K., Wang, K.H., Weitz, C., Whittaker, C., Wilming, L., Wynshaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawaji, H., Kohtsuki, S., and Hayashizaki, Y.
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Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

Nature 420, 563-573 (2002)

B (bases 1 to 2812)

S Adachi, J. Alzawa, K. Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Intoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kowai, J., Kojima, Y., Kondo, S., Konno, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kasukawa, T., Nakazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sasaki, D., Shibaca, K., Shibaca, K., Shibaca, K., Shibaca, K., Shihagawa, A., Shiraki, T., Sogabe, Y., Tangami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Muramatsu, M. and Hayashizaki, Y., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y., Towaru, A., Toya, T., Yasunishi, A., Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The FANTOM Consortium and the RIKEN Genome Exploration Research
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer Genome Res. 10 (11), 1757-1771 (2000)
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Nature 409 (6821), 685-690 (2001)
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|db_xref="taxon:10090"
|clone="C630016P10"
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                       776 AAAATTCAGATTGTCACCCAGATGCTCGAATTGGTGGAGAAACCGAGGGGAGACAAATGGAG 835
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                    896 ATGGATTCCAGTCAAACAGATCTTCTAGAAGACCTCGAAGACAGAGACAGTGAG
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                                                                                LeuHisSerGlnCysPheGlnAspProAlaGluSerGluArgAlaSerAspLysAlaLys
                                                                                                                 140 MetAspSerSerGlnProGluArgSerSerArgArgProArgArgGlnArgThrSerGlu
                                                                                                                                                                                                                                                                                                                                           SerArgAspLeuCysHisMetAlaAsnGly1leGluAspCysAspAspGlnProProLys
                                                                                                                                                                                                                                                                                                                                                                                200 AlaSerProValGluPheAlaIleAspProAsnGluProThrTyrCysLeuCysAsnGln
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y., Arakawa, T., Hara, A., Fukunishi Y., Konno, H., Adachi, J., Fukuda, S., Arakawa, T., Hara, A., Fukunishi Y., Kondo, S., Yamanaka, I., Saito, T., Cajobori, T., Bono, H., Kasukawa, T., Saito, R., Kadota, K., Matsuda, H., Ashburner, M., Batalov, S., Casavant, T., Fleschmann, W., Gaseterland, T., Gissi, C., King, B., Kochiwa, H., Kuchi, P., Lewis, S., Matsuo, Y., Nikaido, I., Pesole, G., Quackenbush, J., Schriml, L.M., Staubli, F., Suzuki, R., Tomita, M., Wagner, L., Washio, T., Sakai, K., Okido, T., Furuno, M., Aono, H., Baldarelli, R., Barsh, G., Blake, J., Beffelli, D., Bojunga, N., Carninci, P., Me Bonaldo, M. P., Brownstein, M. J., Bult, C., Fletcher, C., Fujita, M., Gariboldi, M., Gustincich, S., Hill, D., Hofmann, M., Hume, D.A., Kamiya, M., Lee, N.H., Lyons, P., Nordone, P., Ring, B., Ringwald, M., Rodriguez, I., Sakamoto, N., Sasaki, H.,
                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus 10, 11 days embryo whole body cDNA, RIKEN full-length enriched library, clone:2810011M06 product:inhibitor of growth family, member 1-like, full insert sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chordata, Craniata, Vertebrata, Euteleostomi, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                         260 GlyAspAsnGluLysThrMetAspLysSerThrGluLysThrLysLysAspArgArgSer
                                                                                                                                                                                                                        1259 GGAGACAATGAGAAAACCATGGACAAAAGTACCGAAAAGGACAAAAAGGAGAGAAGAAGGAGG
                                                      PheSerCysValSerLeuThrTyrLysProLysGlyLysTrpTyrCysProLysCysArg
                           ValSerTyrGlyGluMetIleGlyCysAspAsnGluGlnCysProIleGluTrpPheHis
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Mus musculus (house mouse)
Mus musculus
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Mammalia; Eutheria;
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NQVSYGEMIGGDNEQQPIEWFHFSCVSLTYKPKGKWYCPKCRGDNEKTWDKSTEKTKK
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/dev stage="adult"
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                                                                                     /note="unnamed protein product; inhibitor of growth family, member 1-like (MGD|MGI:1916510, GB|NM_023503, evidence: BLASIN, 98%, match=971)
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Mismatches:
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Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

Nature 420, 563-573 (2002)

Be (Dasses I to 1464)

Adachi, J., Aizawa, K., Akahira, S., Akimura, T., Arai, A., Aono, H., Arakwa, T., Bono, H., Carhinci, P., Fukuda, S., Fukunishi, Y., Hramoto, K., Arakwa, T., Bono, H., Carhinci, P., Fukuda, S., Fukunishi, Y., Hramoto, K., Hiraoka, T., Kato, H., Ravai, J., Kojima, Y., Konno, H., Kouda, M., Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Kasukawa, T., Kato, H., Kawai, J., Miyazaki, Y., Okido, H., Casito, H., Saito, R., Ohno, M., Okazaki, Y., Okido, T., Saito, R., Sano, H., Sasaki, D., Saito, H., Saito, R., Sani, C., Sakai, K., Sano, H., Sasaki, D., Shibata, K., Shibata, Y., Shibata, Y., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Tanaka, T., Yoshino, M., Muzamaruki, M. and Hayashizaki, Y., Yoshino, M., Muzamaruki, M. and Hayashizaki, Y., Yoshino, M., Muzamaruk, M. and Hayashizaki, Y., Toya, T., Yasunishi, A., Yoshida, K., Yoshino, M., Muzamaruk, M. and Hayashizaki, Y., Toya, T., Yasunishi, A., Yoshida, K., Shibata, M., Shibata, M., Shibataki, Y., Shibata, M., Shibataki, Y., Toya, T., Yasunishi, A., Yoshida, K., Yoshino, M., Muzamaruki, M., Andayashizaki, Y., Shibata, M., Shibataki, M.,
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| organism="Mus musculus"
| noil_type="mRNA"
| strain="CSTBL/60"
| db_xref="FANTOM_DB:2810011M06"
| db_xref="main="1901365"
| db_xref="main="1901365"
| clone="2810011M06"
| fissue type="whole body"
| clone="15810011M06"
| clone="15810011M06"
| dev_stage="10, 11 days embryo"
| 478. .1322
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Functional annotation of a full-length mouse cDNA collection
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Eukaryota; Merazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.

1 (bases I to 736)
Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E., Fong, W.T., Tickle, C., Brown, W.R.A.; Wilson, S.A. and Hubbard, S.J. A Comprehensive Collection of Chicken CDNAs
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12445392
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603799281F1 CSEQCHN23 Gallus gallus cDNA clone ChEST768a21 5', mRNA
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                    AspMetGlnArgAsnValSerValLeuArgGluLeuAspAsnLysTyrGlnGluThrLeu
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/clone_lib="NIH_MGC_127"
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Site_2: Sfil (ggcgcctcggcc); Double-stranded cDNA was
prepared from a pool of 40 cell line polyA+ RNAs (bladder-2%, blood -33.4%, brain -5.6%, breast -12.5%, colon-4%, connective tissue -1.4%, eye -1%, intestine -2.6%,
/kidnney -2.2%, liver -5.7%, lung -10.8%, NK-cell -5.2%,
/ovary -4%, pDarynx -2.5%, prostate -4.3%, salivary
gland -1.3%, and skin -2.3%). 5' and 3' adaptors were
used in cloning as follows:
5'-AAGAGGGGGGGGGGGAGAGGGGCGATAGGGGGG-3' and
5'-ATTCTAGAGGCCGGGCGCACATGGGT(30)NN-3. Full-length
enriched library was constructed using the Clontech
Creator SMART kit and size-selected to contain the 1-2 kb
size fraction (other fractions present in NIH_MGC_126 and
NIH_MGC_128). Library created in the laboratory of T.
Ubddin, M.D., Ph.D. (NIMH, NIH). Note: this is a NIH_MGC_
Library."
                    DQZ//444 912 bp mRNA linear EST 07-MAY-2002 AGENCOURT_6738254 NIH_MGC_127 Homo sapiens cDNA clone IMAGE:5810745 S', mRNA sequence.
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                                                                                                                                                                        Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 912)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished
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                                                                                                                                                                                                                                                                                  Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: NCI
CDNA Library Preparation: Michael Brownstein Laboratory
CDNA Library Preparation: Michael Brownstein Laboratory
CDNA Library Preparation: Michael Brownstein Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2058 row: h column: 10
High quality sequence stop: 587.
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BQ277444.1 GI:20487652
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1296.00
92.71%
90.62%
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Homo sapiens (human)
Homo sapiens
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Best Local Similarity:
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VERSION
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ORIGIN
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AUTHORS
TITLE
JOURNAL
COMMENT
RESULT 4
BQ277444
LOCUS
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ò 셤 ò us-09-513-365a-1.p2n.rst

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/compatible sites of a custom modified MCS of the
pBluescript (KS+) vector. The library was normalized in 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gallus gallus (chicken)
Gallus gallus
Gallus gallus
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Phasianinae; Gallus.
1 (Bases I to 892)
Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bogch, E.,
Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.
A Comprehensive Collection of Chicken cDNAs
Curr. Biol. 12 (22), 1965-1969 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BU332089 892 bp mRNA linear EST 28-NOV-2002
603869689F1 CSEQCHN65 Gallus gallus cDNA clone ChEST894a23 5', mRNA
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University of Manchester Institute of Science and Technology (UMIST
                                                                                                                                                                 238
                                                                                                                                                                                                       602
                                                                                                                                                                                                                                            HisPheSerCysValSerLeuThrTyrLysProLysGlyLysTrpTyrCysProLysCys 258
                                                                                                                                                                                                                                                                                                                           482
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                          423 AAAGAGAAAAGATCGAAATCTTCCAAGAAAAAAAGGCTCCAAAGCCAAAGAGAGGG
                                                                                                         543 CAAGTGTCTTACGGCGAAATGATAGGATGTGATAACGAACAGTGTCCTATTGAGTGGTTC
      179 LysGluLysLysSerLysSerAlaLysLysLysLysArgSerLysAlaLysGlnGluArg
                                                                                   GlualaSerProValGluPheAlaIleAspProAsnGluProThrTyrCysLeuCysAsn
                                                                                                                                                                                                                                                                                    603 cactrictografitagacticacctaraaaccgaaggggaarggrafitgccccaagrac
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    .892
    /organism="Gallus gallus"

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PO Box 88, Manchester, M60 1QD,
Tel: 01612008930
Fax: 01612360409
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BU332089
BU332089.1 GI:25840090
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                                                                                                                                                                                                                                                                                                                                                                                                            SerArg 280
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//dev stage="12"
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ECORI; Site_2: Not!; This normalized library was
constructed from 1 million independent clones. cDNA
synthesis was initiated using an oligo(dT) primer, using
methylated C in the first strand synthesis reaction.
Following this first strand reaction, double-stranded cDNA
was blunted, ligated to NotI adapters, digested with EcoRI
comparible sites of a custom modified MCS of the
pBluescript (KS+) vector. The library was normalized in 2
rounds using conditions adapted from Soares et al., PNAS
(1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6
(1996): 791, except that a significantly longer
reannealing hybridization was used."
                                         of Science and Technology (UMIST
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Conservative:
Mismatches:
Indels:
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Contact: Simon Hubbard
Department of Biomolecular Sciences
University of Manchester Institute o
                                                                          PO Box 88, Manchester, M60 1QD, UK
Tel: 01612008930
Fax: 01612360409
Email: Simon.Hubbard@umist.ac.uk.
                                                                                                                                                                                              /organism="Gallus gallus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps:
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92.98%
85.95%
75.83%
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1. 919
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| /mol_type="minA" |
| /mol_type="minA" |
| /db xref="taxon:9606" |
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| /clone="See 'Creation of Genome-wide Protein Expression |
| /note="See 'Creation of Genome Activation of Genome Biotechnology, in press. Note that even though the cell type indicated is HT1080 since a random activation method was used, these sequence tags are not necessarily expressed in HT1080 under normal circumstances."
                                                                         Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases I to 919)

1 (bases I to 919)

Cain,S., Leventhal,C., Thornton,M., Ramachandran,R., Whittington,J., Lerner,L., Costanzo,D., McElligott,K., Boozer,S., Mays,R., Smith,E., Veloso,N., Klika,A., Hess,J., Cothren,K., Lo,K., Offenbacher,S., Danzig,J. and Ducar,M.

Creation of genome-wide protein expression libraries using random activation of gene expression

Mat. Biotechnol. 19 (5), 440-445 (2001)
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Fax: 216 361 9596
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Location/Qualifiers
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                 GI:13733231
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Contact: Scott J. Cain
Athersys, Inc.
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rounds using conditions adapted from Soares et a (1994) 91: 9228-9232 and Bonaldo et al., Genome (1996): 791, except that a significantly longer reannealing hybridization was used."
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Matches:
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Mismatches:
Indels:
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93.06%
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Alignment Scores: 3.37e-61 Length: 793 Pred. No.: 1094.00 Matches: 224 Score: 1094.00 Matches: 224 Percent Similarity: 97.82\$ Mismatches: 4 Query Match: 10 Gaps: 0 Best Local Similarity: 97.82\$ Indels: 3 DB: US-09-513-365A-1 (1-280) x BE796780 (1-793)	1 MetteuGlyglnGlnGlnGlnCenTyrSerSerAlaAlaLeuLeuThrGlyGluArg 20 	21 SerArgLeubeuThrCysTyrValGlnAspTyrLeuGluCysValGluSerLeuProHis 40 	41 AspMetGlnArgAsnValSerValLeuArgGluLeuAspAsnLysTyrGlnGluThrLeu 60 	61 LysGluileAspaspValTyrGluLysTyrLysLysGluAspAspLeuAsnGlnLysLys 80 	10	101 IleGInIleValThrGlnMetLeuGluLeuValGluAsnArgAlaArgGlnMetGluLeu 120 	121 HisserGlncysPheGlnAspProAlaGluSerGluArgAlaSerAspLysAlaLysMet 140 	141 AspSerSerGlnProGluArgSerSerArgArgProArgArgGlnArgThrSerGluSer 160 	161 ArgAspLeu-CysHisMetAlaAsnGlyIleGluAspCysAspAspGlnProProLysGl 180 	180 ulyslysSerlysSeralalyslyslyslysrgserlysalalysglngluargglual 200 	200 aSerProValGluPheAlalleAspProAsnGluProThrTyrcysLeuCysAsnGlnVa 220	220 lSerTyrGlyGluMetIleGlyCys 228 767 GTCTTG-GGGGAGATGATAATGGGTGT 790	<u></u>	mRNA sequence	URCE Homo sapiens (human) ORGANISM Homo sapiens Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. FERENCE 1 (bases 1 to 778)	AUTHORS NIH-MGC http://mgc.nci.nih.gov/. TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
Align Pred. Score Score Perce Best Query DB: US-09	& 8	& 8	\$ a	8 %	ò a	& 8	b o	දුරු පු	\$ 8	& 8	\$ 65	oy Op	RESULT S BI548536 LOCUS DEFINIT	ACCES VERSI KEYW	SOURC	AUT TIT
304 AGTGAAAGCCGTGATTTATGTCACATGGCAAATGGGATTGAAGACTGTGATGAGCCA 363 178 ProLysGluLysLysSerLysSerAlaLysLysLysLysArgSerLysAlaLysGlnGlu 197	218 ASRGINVALSETTYRG1yG1wMetileG1yCysAspAsrGluGlnCysProileG1uTrp 237	238 PhehisPheSerCysValSerLeuThrTyrLysBroLysGlyLysTrpTyrCysProLys 257	258 CysargdlyaspabnglulysThrmetasplysSerThrdlulysThrlysLys 275 ::	276 Aspargargserarg 280 	Z		X.	Tammara, Description of The Control	чыос	G (COUNT ATTROUGN THE 1.M.A.5. CORBORTIUM/LLNL AT: IMAGE.LIF Plate: LLCM794 row: a column: 16 High quality sequence stop: 769. Location/Qualifiers		/clone="IMACE:3941655" /tissue_type="small cell carcinoma" /cell_line="MGC3" /lab_host="DHJO8 (phage-resistant)" /clone_lib="NIH MGC 7"	/note="Organ: lung; Vector: pOTB7; Site_1: Xho1; Site_2:	insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."	
8 & 8 & 8 8 & 8 & 8	oy O	, da	oy Ob	cy G	RESULT 8 BE796780 LOCUS DEFINITION	ACCESSION VERSION	SOURCE ORGANISM	REFERENCE AUTHORS TITLE	COMMENT		FEATURES			: <u>:</u>	BASE COUNT	ORIGIN

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BU259874 779 bp mRNA linear EST 26-NOV-2002 603504254F1 CSEQCHN51 Gallus gallus cDNA clone ChEST426k14 5', mRNA sequence.
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Department of Biomolecular Sciences
University of Manchester Institute of Science and Technology (UMIST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 (bases 1 to 779)
Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E., Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.
A Comprehensive Collection of Chicken cDNAs
Curr. Biol. 12 (22), 1965-1969 (2002)
                                                                                                                               604 CGTGATTTATCTCACATGCCAAATGCGATTGAAGACTGTGATGATGATCAGCCACCTAAAGAA 663
                                                                                                                                                                                       LysLysSerLysSerAlaLysLysLysLysArgSerLysAlaLysGlnGluArgGluAla 200
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Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Archosauxia; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
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Tel: 01612008930
Fax: 01612360409
Email: 8imon.Hubbard@umist.ac.uk.
Location/Qualifiers
1. 779
/organism="Gallus gallus"
/mol type="mRNA"
/gtrain="Mhite Leghorn, Hisex"
/db xref="texon:9031"
/clone="ChEST426k14"
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/lab_host="DH10B"
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/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="InAGE:526240"

/tissue_type="hippocampus"

/tab_nost="DH108"

/clone lib="NNH MGC 95"

/clone lib="NNH"

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                                                     Email: cgapbs-remail.nih.gov

Tissue Procurement: Miklos Palkovits, M.D., Ph.D.

CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
Toshiyuki and Piero Carninci (RIKEN)

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Inotyte Genomics; Inc.

Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLAMI1661 row: n column: 13

High quality sequence stop: 775.

Location/Qualifiers
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Matches:
Conservative:
Mismatches:
                                 Contact: Robert Strausberg, Ph.D.
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/deverage=1301123
/deverage=1301123
/deverage=1301103
/lab_host="NathOB"
/lab_host="NathOB"
/cone_11b="CSEQCHN5"
/note="Organ: trunks; Vector: pBluescript II KS(+);
Site 1: EcoRI; Site 2: Not1; This normalized library was
constructed from 1 million independent clones. cDNA
synthesis was initiated using an oligo(dT) primer, using
methylated C in the first strand synthesis reaction.
Following this first strand reaction, double-stranded cDNA
was blunted, ligated to NotI adapters, digested with EcoRI
compatible sites of a custom modified MCS of the
pBluescript (KS+) vector. The library was normalized in 2
rounds using conditions adapted from Soares et al., PNAS
(1994) 91: 9228-9212 and Bonaldo et al., Genome Research 6
(1996): 791, except that a significantly longer
reannealing hybridization was used."
 University of Manchester Institute of Science and Technology (UMIST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     uAsnArgAlaArgGlnMetGluLeuHisSerGlnCysPheGlnAspProAlaGluSerGl 132
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      72 sGluAspAspLeuAsnGlnLysLysArgLeuGlnGlnLeuLeuGlnArgAlaLeuIleAs
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Matches:
Conservative:
Mismatches:
                                                                                                                            /organism="Gallus gallus"
/mol_type="mRNA"
/strain="White Leghorn, Hisex"
                  )
PO Box 88, Manchester, M60 1QD, UI
Tel: 01612008930
Fax: 01612360409
Email: Simon.Hubbard@umist.ac.uk:
Location/Qualifiers
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/clone="ChEST531f23"
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92.86%
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Best Local Similarity:
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IS31f23 5', mRNA
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Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E., Rong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J. A Comprehensive Collection of Chicken cDNAs
Curr. Biol. 12 (22), 1965-1969 (2002)
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Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                GluIleAspAspValTyrGluLysTyrLysLysGluAspAspLeuAsnGlnLysLysArg
                                                                                                                                GAAATAGACGACGTCTATGAAAAATACAAGTCTGAGAACGATCCTGCTCAGAAGAAACGC
                                                                                                                                                                                               TIGCAGCAGCACCTCCAGCGGGCTTTAATCAACAGTCAAGAACTCGGAGAGATGAAAATT
                                                                                                                                                                                                                                       Gln11eValThrGlnMetLeuGluLeuValGluAsnArgAlaArgGlnMetGluLeuHis
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603581891F1 CSEQCHN75 Gallus gallus CDNA clone ChEST531f23
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 Conservative:
Mismatches:
Indels:
Gaps:
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Department of Biomolecular Sciences
                                                                             US-09-513-365A-1 (1-280) x BU259874 (1-779)
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BU386788
BU386788.1 GI:25894789
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Gallus gallus
 94.06%
88.13%
70.43%
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Percent Similarity:
Best Local Similarity:
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BU386788
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AUTHORS
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BU323498
603489003F1 CSEQCHN63 Gallus gallus cDNA clone ChEST388e2 5', mRNA
I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is CTGCTCAGGT.

TAG IISBUT-CF-EN1

TAG IISBUE-Human Lung Epithelial Cell Lines untreated LPS 6hr to LPS 2h

TAG SEQ=CTGCTCAGGT"

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Gallus gallus (chicken)
Gallus gallus
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   171 GludspCysAspAspGlnProProLysGluLysLysSerLysSerAlaLysLysLysLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GluProThrTyrCysLeuCysAsnGlnValSerTyrGlyGluMetIleGlyCysAspAsn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            111 ValGluAsnArgAlaArgGlnMetGluLeuHisSerGlnCysPheGlnAspProAlaGlu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GluGlnCysProlleGluTrpPheHisPheSerCysValSerLeuThrTyrLysProLys
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Conservative:
Mismatches:
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/lab_host="DH10B (Life Technologies) (T1 phage resistant)"

/clonellib="ULCF-ENI"

/note="Organ: Lung; Vector: pT773-pac (Pharmacia) with a
modified polylinker; Site_1: EcoR I; Site_2: Not I;
UL-CF-ENI is a normalized cDNA library containing the
following tissue(s): Primary Lung Cystic Fibrosis
Epithelial Cells. The library was constructed according to
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. First strand cDNA synthesis was primed with an
oligo-dT primer containing a Not I site. Double stranded
CDNA was ligated to an EcoR I adaptor, digested with Not
                                                                                                                                                                                                                                                                                                                                                                                                        BM982877 1735 bp mRNA linear EST 21-FEB-2003 UI-CF-EN1-acs-d-05-0-UI.SI UI-CF-EN1 Homo sapiens cDNA clone UI-CF-EN1-acs-d-05-0-UI 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                University of Iowa
University of Iowa
2024 University of Iowa Med Labs, Iowa City, IA 52242, USA
Tel: 319 356 4866
Fax: 319 356 7171
Email: paul-mccray@niowa.edu
Tissue Procurement: Dr. M. J. Welsh, University of Iowa
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
DNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.resgen.com) or from Open Biosystems
                                                                                  541
                                                                                                                         232
                                                                                                                                                               601
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Bonaldo, M.F., Lennon, G. and Soares, M.B.
Normalization and subtraction: two approaches to facilitate gene
                                                                                                                                                                                                      CTGCGACGATCAGCCACCTAAAGAGAAAAGATCGAAATCTTCCAAGAAGAAAAACGCTC
                                         rLysAlaLysGlnGluArgGluAlaSerProValGluPheAlaIleAspProAsnGluPr
                                                                                                                                                GACTTACTGCTTATGTAACCAAGTGTCTTACGGCGAAATGATAGGATGTGATAACGAACA
                                                                                CAAAGCCAAACAAGAGGGAGGTTTCACCCGTGGAGTTTGCGATTGATCCAATGAACC
                                                                                                                       OThrTyrCysLeuCysAsnGlnValSerTyrGlyGluMetIleGlyCysAspAsnGluGl
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/db_xref="taxon:9606"
/clone="UI-CF-ENN-acs-d-05-0-UI"
/tissue_type="Primary Lung Cystic Fibrosis Epithelial
Cells"
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/organism="Homo sapiens"
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Seg primer: M13 FORWARD
POLYA=Yes.
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Homo sapiens
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150

556

616

170

496

190

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//db_xref="mRNA"
//db_xref="mRNA"
/db_xref="mRNA"
/db_xref="mRNA"
/clone="Index[s:6430226"
/lab host="mRIH_MGC_137"
/clone=lib="NIH_MGC_137"
/clone=lib="NIH_MGC_137"
/note="Organ: pancreas; Vector: pSPORTI; Site 1: SalI;
Site_2: NotI; Library consists of a pool of clones
rearrayed from the following libraries: Melton normalized
mixed mouse pancreas 1 N1-MMSI, Amplified Melton mouse
isletes 1 MISI-A, and Kaestner ngn3 wt. Clones rearrayed in
the laboratory of K. Kaestner (University of Pennsylvania
). Note: this is a NIH MGC Library."
37 a 217 c 161 g 289 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          864 bp mRNA linear EST 20-SEP-2002
AGENCOURT_8866651 NIH_MGC_137 Mus musculus cDNA clone IMAGE:6430926
5', mRNA sequence.
BU591073
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11 H-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished
                                                                                                                   375 GGCCAAGATGGAGTCCTGCCAGCCAGAGATCATCACCTAGACCTCGTCGGCAGCGAAC
                                                                                                                                                        rSerGluSerArgAspLeuCysHisMetAlaAsnGlyIleGluAspCysAspAspGlnPr
                                                                                                                                                                                                                                        DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.B. Consortium/LLNL at:
http://image.llnl.gov.a column: 07
                                                    315 GATGGAAACACTCTCAGTGTTTTCAGGATCTGTCTGAAAACGACAAGCCTCTGGAAAA
                                                                                  OProLysGluLysLysSerLysSerAlaLysLysLysLysArgSerLysAlaLysGlnGl
                                                                                                                                                                                                                                                                                           uArgGluAlaSerProValGluPheAlaIleAspProAsnGluProThrTyrCysLeuCy
                                                                                                                                                                                                                                                                                                                                                            217 sAsnGlnValSerTyrGlyGluMetIleGlyCysAspAsnGluGlnCysProIleGluTr
                     nMetGluLeuHisSerGlnCysPheGlnAspProAlaGluSerGluArgAlaSerAspLy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Robert Strausberg, Ph.D.
Bmail: cgapbs-r@mail.nih.gov
Tissue Prccurrement: Gerard Gradwohl (PNAS 97 P1607-1611, 2000)
CDNA Library Preparation: Catherine Lee, Endocrine Pancreas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Consortium cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                                                                                                                                                                                                                                                                                                                                                                                                                               237 pPheHisPheSerCysValSerLeuThrTyr 247
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/organism="Mus musculus"
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Location/Qualifiers
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Mus musculus
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Department of Biomolecular Sciences
University of Manchester Institute of Science and Technology (UMIST
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
1 (bases 1 to 707)
Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, B.,
Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.
Cuprehensive Collection of Chicken cDNAs
Cuprehensive (22), 1965-1969 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    117
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Mismatches:
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Gaps:
                                                                                                                                                                                                                     PO Box 88, Manchester, M60 1QD, UK
                                                                                                                                                                                                                                     Tel: 01612008930
Fax: 01612360409
Email: Simon.Hubbard@umist.ac.uk.
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91.77%
84.42%
69.01%
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Best Local Similarity:
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 Cain, S., Leventhal, C., Thornton, M., Ramachandran, R., Whittington, J., Lerner, L., Costanzo, D., McBlligott, K., Boozer, S., Mays, R., Smith, E., Veloso, N., Klika, A., Hess, J., Cothren, K., Lo, K., Offenbacher, J., Danzig, J. and Ducar, M. Creation of genome-wide protein expression libraries using random Cativation of gene expression

Nat. Biotechnol. 19 (5), 440-445 (2001)
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3201 Carnegie Ave, Cleveland, C
Tel: 216 431 9900
Fax: 216 361 9596
Email: scalin@athersys.com
High quality sequence stop: 531
                                                                                                                                 Cleveland,
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Bukaryota: Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 798)
Harrington, J.J., Sherf, B., Rundlett, S., Jackson, P.D., Perry, R.,
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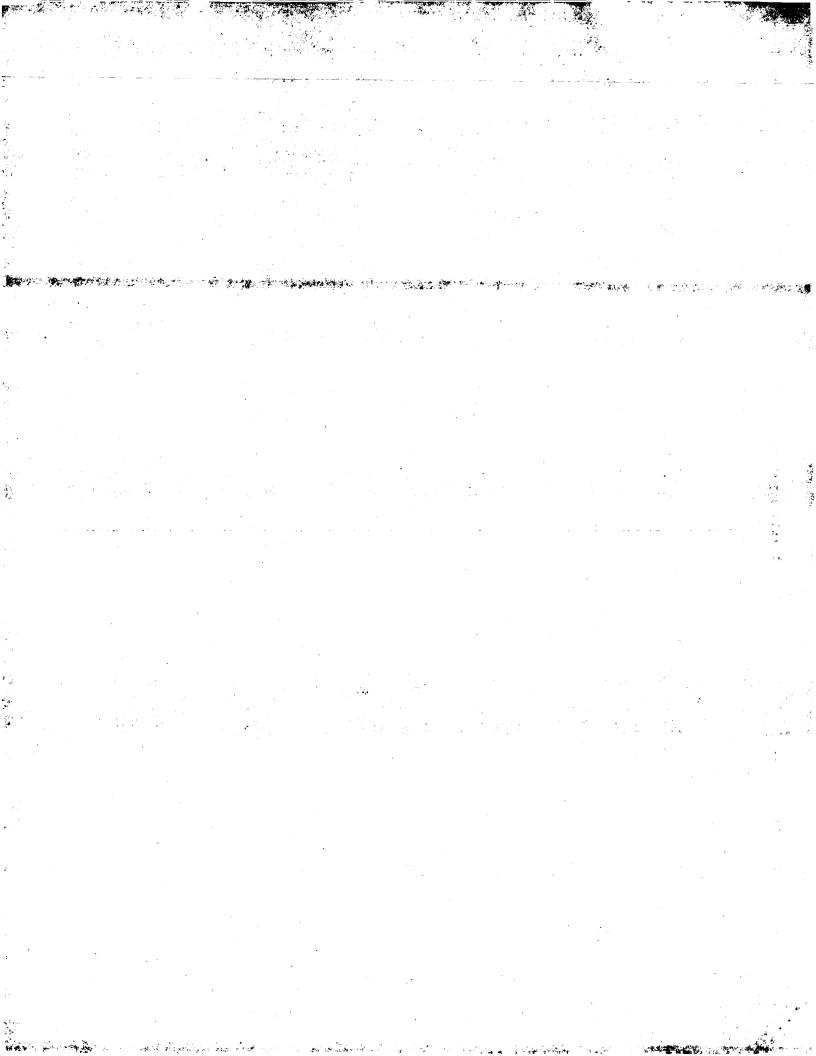
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GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd. OM protein - nucleic search, using frame_plus_p2n model Run on: January 12, 2004, 19:24:44 ; Search time 77 Seconds (without alignments)	DNE	seqs, 220691566 r itisfying chosen p 0 2000000000 um Match 0% um Match 100%	Command line parameters: -MODEL=frame+ p2n.model -DEV=xlp -Q=(cgn2_1/USPTC spool_p/US09513365/runat_12012004_163932_28784/app_query.fasta_1.455 -Q=(cgn2_1/USPTC spool_p/US09513365/runat_12012004_163932_28784/app_query.fasta_1.455 -DB=Issuede Patents NA -QFMT=fastap -SUFFIX=p2n.rni -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL_OUTFMT=pto -NORM=ext -HERAPSIZE=500 -MINLENG=0 -MAXLENS=2000000000 -USER=US09513365_@CGN 1 1 103 @runat_12012004 163932_28784 -NCPU=6 -ICPU=3 -NO MMAP -LARGEQUERY -NEG_SCORES=0 -WALT -DSPBLOCK=100 -LONGLOG -DBV_TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -PGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7	e: Issued_Patents_NA:* 1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:* 2: /cgn2_6/ptodata/2/ina/6B_COMB.seq:* 3: /cgn2_6/ptodata/2/ina/6B_COMB.seq:* 4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:* 5: /cgn2_6/ptodata/2/ina/6B_COMB.seq:* 6: /cgn2_6/ptodata/2/ina/pcTuS_COMB.seq:* 6: /cgn2_6/ptodata/2/ina/pcTuS_COMB.seq:* 6: /cgn2_6/ptodata/2/ina/packfIles1.seq:*	r than or equal to the score of the result being print SUMMARIES ETY CONTROL IN ID CONTROL IN ID CONTROL IN IN INC. INC. INC. INC. INC. INC. INC	728 49.2 1902 3 US-09-258-372-1 Sequence 1, 728 49.2 2061 2 US-09-258-371-9 Sequence 9, 728 49.2 2061 3 US-08-751-230-9 Sequence 9,

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272 AAGGAAATTGATGATGTCTACGAAAATATAAAGAAAGAAGAGATGATTTAAACCAGAAGAAA
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                                                                         OTHER INFORMATION: human
 PatentIn Ver.
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  MetLeuGlyGlnGlnGlnGlnGlnLeuTyrSerSerAlaAlaLeuLeuThrGlyGluArg
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US-09-601-478-7

Squence 7, Application US/09601478

Patent No. 6403785

GRENEAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION: Human TSC403 gene and human INGIL gene
TITLE REFERENCE: 060193

CURRENT APPLICATION NUMBER: US/09/601,478

CURRENT FILING DATE: 1900-08-03

PRIOR FILING DATE: 1998-04-28

PRIOR FILING DATE: 1998-03-05

PRIOR APPLICATION NUMBER: JP H10-73234

PRIOR FILING DATE: 1998-03-05

PRIOR APPLICATION NUMBER: JP H10-33133

PRIOR APPLICATION NUMBER: JP H10-38133

NUMBER OF SEQ ID NOS: 11
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	Db 907 GGGGAAAATGGTATTTGCCCCAAAGGGGGGGGAAAATGGAAAAAGGAAAATGGAGGGGGGG
QY 261 AspAsnGluLysThrMetAspLysSerThrGluLysThrLysLysAspArgArgAsgargSerArg 280	< A A A A A A A A A A A A A A A BEGGGGH I

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116 ArgGlnMetGluLeuHisSerGlnCysPheGlnAspProAlaGlu------
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Best Local Similarity:
Query Match:
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US-09-258-257-1
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                    Gaps:
                                                                                                                                     6.3e-86
853.50
75.74%
59.19%
57.63%
STRANDEDNESS: single
            TOPOLOGY: linear MOLECULE TYPE: CDNA
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                                                                                                                                                                  Percent Similarity:
Best Local Similarity:
                                                          ; NAME/KEY: CDS
; LOCATION: 7...(
US-09-006-783A-4
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Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Burns, Doane, Swecker & Mathis STREET: P.O. Box 1404
CITY: Alexandria STATE: Virginia COUNTRY: United States
ZIP: 22313-1404
COMPUTER: READBALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-513-365A-1 (1-280) x US-09-258-257-1 (1-1902)
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Matches:
Sequence 1, Application US/09258257
Patent No. 596398
GENERAL INFORMATION:
APPLICANT: RIABOWOL, Karl
TITLE OF INVENTION: SUPPRESSOR GENE
TITLE OF INVENTION: SUPPRESSOR GENE
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOUTWARE: Patentin Release #1.0, Ve. CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/258,257 FILLNG DATE:
CLASSIFICATION TO DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 08/569,721 FILING DATE: 08-DEC-1995
ATTORNEY/ACENT INFORMATION:
NAME: MOOI, Leslie A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ALICKANIA MAMBE MOOJ, LGEBLIE A.
REGISTRATION NUMBER: 37,047
REFERENCE/DOCKET NUMBER: 02877
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 854-7400
TELEPHONE: (650) 854-8275
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1902 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
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74.79%
58.12%
49.16%
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1902 136 39 45 14

Matches: Conservative: Mismatches: Indels:

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US-09-513-365A-1 (1-280) x US-09-258-371-1 (1-1902)
                                                                                                                                                             728.00
74.79%
58.12%
49.16%
   nucleic acid
EDNESS: double
                                                                        CDS
109..741
                               TOPOLOGY: linear MOLECULE TYPE: CDNA
                                                                                                                                                                         Percent Similarity:
Best Local Similarity:
                  STRANDEDNESS:
                                                                      , NAME/KEY:
, LOCATION:
US-09-258-371-1
                                                                                                                                   Alignment Scores:
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                                                            FEATURE
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                                                                                                   GCGTCCAGCAACCACGACCACGACGCGCCTCGGGCACCAAGGAGAAGAAGAAGGAGCC 444
                                                                                                                                                                                                     LysSerAlaLysLysLysArgSerLysAlaLysGlnGluArgGluAlaSerProVal 203
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CGGCAGGTGGACACCACGTGGAGCTGTTCGAGGCGCAGCAGGAGCTGGGCGACACAGTG 270
                                                                                    144 GlnProGluArgSerSerArgArgProArgArgGlnArgThrSerGluSerArgAspLeu 163
                                                                                                                                            164 CysHisMetAlaAsnGlyIleGluAspCysAspAspGlnProProLysGluLysLysSer 183
                            -----SerGluArgAlaSerAspLysAlaLysMetAspSerSer
                                                                                                                                                                                                                        GluPheAlaIleAspProAsnGluProThrTyrCysLeuCysAsnGlnValSerTyrGly
                                                                                                                                                                                                                                                                               GluMetIleGlyCysAspAsnGluGlnCysProlleGluTrpPheHisPheSerCysVal
                                                                                                                                                                                                                                                                                                                                                   SerLeuThrTyrLysProLysGlyLysTrpTyrCysProLysCysArgGlyAspAsnGlu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1, Application US/09258371
Patent No. 5986078
GENERAL INFORMATION:
APPLICANT: Garkavtsev, Igor
APPLICANT: Riabowol, Karl
TITLE OF INVENTION: DNA SEQUENCE ENCODING THE TUMOR
TITLE OF INVENTION: SUPPRESSOR GENE ING1
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Burne, Doane, Swecker & Mathis STREET: 699 Prince Street
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/258,371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/751,230
FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Mool, Lealie A.
REGISTRATION NUMBER: 37,047
REFRENCE/DOCKET NUMBER: 0287:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-854-7400
TELEFAX: 415-854-875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 415-854-8275
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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151 CTGGGCGACGAGAAGATCCAGATCGTGAGCCAGATGGTGGAGCTGGTGGAGAACCGCACG 210
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                                                                                                  56 TyrGlnGluThrLeuLysGluIleAspAspValTyrGluLysTyrLysLysGluAspAsp
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GENERAL INFORMATION: APPLICANT: GARKAVISEV, Igor
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244 SerieuThrTyrLysProLysGlyLysTrpTyrCysProLysCysArgGlyAspAsnGlu 263
164 CysHisMetAlaAsnGlyIleGluAspCysAspAspGlnProProLysGluLysLysSer 183
                                                                         LysSerAlaLysLysLysLysArgSerLysAlaLysGlnGluArgGluAlaSerProVal 203
                                                                                                                                                     204 GluPheAlaIleAspProAsnGluProThrTyrCysLeuCysAsnGlnValSerTyrGly 223
                                                                                                                                                                                                                                                                                                                                385 GCGTCCAGCAACCACGACCACGACGACGCCCTCGGGCACACCCAAGGAGAAGAAGGACC
                                                                                               GluMetIleGlyCysAspAsnGluGlnCysProIleGluTrpPheHisPheSerCysVal
                                                                                                                                                                                                                                                    264 LysThrMetAspLysSerThrGluLysThrLysLysAspArg 277
                                                                                                                                                                                                                                                                                                                                                                                                           Version #1.30
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STREET: 699 Prince Street
CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Garkavtsev, Igor
APPLICANT: Garkavtsev, Igor
APPLICANT: Riabowol, Karl
TITLE OF INVENTION: DNA SEQUENCE ENCODIN
TITLE OF INVENTION: SUPPRESSOR GENE ING1
NUMBER OF SEQUENCES: 23
CORRESPONDENCES: ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Rloppy disk
COMPUTER: READABLE FORM:
MEDIUM TYPE: Rloppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: DatentIn Release #1.0, Ver
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/751,230
FILING DATE: 15-NOV-196
CLASSIFFCATION: S14
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/569721
FILING DATE: 08-DEC-1995
ATTORNEY/AGENT INFORMATION:
NAME: MOOI, Leslie A.
REGISTATION NUMBER: 37,00772
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1, Application US/08751230 Patent No. 6117633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE DOCKET NUMBER: 02
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-854-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 415-854-8275
INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 1902 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA
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LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          116 ArgGlnMetGluLeuHisSerGlnCysPheGlnAspProAlaGlu-----
                                                                                       CARDERSER: Burns, Doone, Swecker & Mathis STREET: P.O. Box 1404

CITY: Alexandria
COUNTRY: United States
ZIATE: United States
ZIP: 22313-1404

COMPUTER READBLE FORM:
MEDIUM TYPE: FLOSPY disk
COMPUTER: IBM PC compatible
OFFRATING SYSTEM: PC-DOS/MS-DOS
SOFFWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/569,721A
FILING DATE: 08-DEC-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
             DNA SEQUENCE ENCODING A TUMOR SUPPRESSOR GENE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-513-365A-1 (1-280) x US-08-569-721A-1 (1-1902)
                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Mooi, Leslie A.
REGISTRATION NUMBER: 37,047
REFERENCE/DOCKET NUMBER: 028722-128
TELECOMMUNICATION: INFORMATION:
TELEPHONE: (650) 854-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (650) 854-8275
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1902 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           74.79$
58.12$
49.16$
                 TITLE OF INVENTION: DN
TITLE OF INVENTION: SU
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; NAME/KEY:
; LOCATION:
US-08-569-721A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Alignment Scores:
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164 CysHisMetAlaAsnGlyIleGluAspCysAspAspGlnProProLysGluLysLysSer 183
                                                                                                                                                                                              PRICE APPLICATION DATA:
APPLICATION NUMBER: US/08/828,158
FILING DATE: 27-MAR-1997
APPLICATION NUMBER: US 08/751230
FILING DATE: 15-NOV-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/569721
FILING DATE: 08-DEC-1995
ATTORNEY/AGENT INFORMATION:
NAME: MOOI, Leslie A.
REGISTRATION NUMBER: 37,0477
                    ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ve:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/499,082
                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 02
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-854-7400
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SEQUENCE CHARACTERISTICS:
LENGTH: 1902 base pairs
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74.79%
58.12%
49.16%
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STRANDEDNESS: double
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Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                FILING DATE:
CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; LOCATION:
US-09-499-082-1
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                                                                                                                                                             56 TyrGlnGluThrLeuLysGluIleAspAspValTyrGluLysTyrLysLysGluAspAsp
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APPLICANT: Riabowol, Karl
APPLICANT: Johnston, Randall N.
APPLICANT: Johnston, Randall N.
APPLICANT: Johnston, METHODS OF MODULATING APOPTOSIS
NUMBER OF SEQUENCES: 23
CORRESPONDENE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: 699 Prince Street
CITY: Alexandria
STATE: VA
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   1902
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 Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                           US-09-513-365A-1 (1-280) x US-08-751-230-1 (1-1902)
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Patent No. 6143522
1.94e-71
728.00
74.79%
58.12%
49.16%
                                   Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
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                                                                        Query Match:
DB:
     Pred. No.:
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Version #1.30
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Matches:
Conservative:
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                       Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Garkavtsev, Igor
APPLICANT: Riabowol, Karl
TITLE OF INVENTION: DNA SEQUENCE ENCODIN
TITLE OF INVENTION: SUPPRESSOR GENE INGI
NUMBER OF SEQUENCES: 23
CORRESPONDENCES ADDRESSS:
ADDRESSEE: Burns, Doane, Swecker & Mat
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; Sequence 9, Application US/09258371
; Patent No. 5986078
     728.00
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rercent Similarity:
Best Local Similarity: !
Query Match:
DB:
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ZIP: 22313-1404
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                                                                                                                                  204 GluPheAlaIleAspProAsnGluProThrTyrCysLeuCysAsnGlnValSerTyrGly 223
                                                                                                                                                        244 SerLeuThrTyrLysBroLysGlyLysTrpTyrCysProLysCysArgGlyAspAsnGlu 263
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                                                                                          445 AAGACCTCCAAGAAGAAGAAGCGCTCCAAGGCCAAGGCGGAGAGGGGGGGCCCCTGCC
                                                                                                                                                                                                        224 GluMetIleGlyCygAspAsnGluGlnCysProIleGluTrpPheHisPheSerCysVal
       385 GCGTCCAGCAACCACGACCACGACGACGCGCTCGGGCACACCCAAGGAGAAGGCC
                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Garkavtsev, Igor
APPLICANT: Riabowol, Karl
TITLE OF INVENTION: DNA SEQUENCE ENCODING THE TUMOR
TITLE OF INVENTION: SUPPRESSOR GENE ING1
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: 699 Prince Street
CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                 264 LysThrMetAspLysSerThrGluLysThrLysLysAspArg 277
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: VA
COUNTRY: USA
ZID: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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CLASSIFICATION:
PRIOR APPLICATION
APPLICATION NUMBER: 08/751,230
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1, Application US/09258372
Patent No. 6238918
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: Mooi, Leslie A.
REGISTRATION NUMBER: 37,047
REFRENCE/DOCKET NUMBER: 0287
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-854-8275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 1:
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TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA
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LOCATION: 109
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Pred. No.:
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244 SerLeuThrTyrLysProLysGlyLysTrpTyrCysProLysCysArgGlyAspAsnGlu 263
                                                                                    224 GlumetileGlyCygAspAsnGluGlnCysProlleGluTrpPheHisPheSerCysVal 243
                                                                                                           784 GGGCTCAATCATAAACCCAAGGGCAAGTGGTACTGTCCCAAGTGCCGGGGGGGAGAACGAG 843
204 GlupheAlaileAspProAsnGluProThrTyrCysLeuCysAsnGlnValSerTyrGly 223
                                       664 GACCTCCCCATCGACCCAACGAACCCACGTACTGTCTGCAACCAGGTCTCCTATGGG
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APPLICANT: Riabowol, Karl
TITLE OF INVENTION: DNA SEQUENCE ENCODING THE TUMOR
TITLE OF INVENTION: SUPPRESSOR GENE INGI
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
STREET: 699 Prince Street
CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER REALMANDE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/751,230
FILING DATE: 15-NOV-1996
CLASSIPICATION 1514
PRIOR APPLICATION NUMBER: US/8/569721
PILING DATE: 08-DEC-1995
ATTONNEY/AGENT INPORMATION:
NAME: MOOI, Leslie A.
REGISTRATION NUMBER: 37,047
REFERENCE/DOCKET NUMBER: 37,047
REFERENCE/DOCKET NUMBER: 37,047
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFRAK: 415-854-7400
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Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                             ; Sequence 9, Application US/08751230; Patent No. 6117633; GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
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ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: CDNA
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Best Local Similarity:
Query Match:
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; LOCATION: 16.
US-08-751-230-9
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US-08-751-230-9
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136
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         COMPUTER: IBM PC Compatible COMPUTER: IBM PC Compatible COMPUTER: IBM PC Compatible COMPUTER: IBM PC Compatible COMPUTER: IBM PC COMPUTED: CONFIDENCE: PATENTIN BATA: APPLICATION NUMBER: US/09/258,371
FILING DATE: PAPLICATION DATA: APPLICATION NUMBER: 08/751,230
FILING DATE: ATTORNEY/AGENT INFORMATION: APPLICATION NUMBER: 37,047
REFERENCE/COMPUTER: 37,047
REFERENCE/COMPUTED: 115-954-7400
TELEFAK: 415-954-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative:
Mismatches:
Indels:
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74.79%
58.12%
49.16%
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STRANDEDNESS: double
COMPUTER READABLE FORM:
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US-09-258-371-9
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Best Local Similarity:
Query Match:
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Matches:
Conservative:
Mismatches:
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                               CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/628,158
FILING DATE: 27-MAR-1997
APPLICATION NUMBER: US 08/751230
FILING DATE: 15-NOV-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/569721
FILING DATE: 08-DEC-1995
ATTORNEY/AGENT INFORMATION:
NAME: MOOI, Leslie A.
REGISTRATION NUMBER: 37,047
REGISTRATION NUMBER: 37,047
REGISTRATION NUMBER: 028722-14;
TELEPHONE: 650-854-7400
TELEPHONE: 650-854-7400
TELEPHAX: 650-854-8275
INFORMATION FOR SECIED NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 2061 base pairs

"WIND: MICHAEL ACID
US/09/499,082
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728.00
74.79%
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STRANDEDNESS: double
TOPOLOGY: linear
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16..900
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Best Local Similarity:
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LOCATION:
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DB:
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                   TyrGlnGluThrLeuLysGluIleAspAspValTyrGluLysTyrLysLysGluAspAsp
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APPLICANT: Riabowol, Karl
APPLICANT: Riabowol, Karl
APPLICANT: Conneton, Randall N.
APPLICANT: Garkavtsev, Igor
TITLE OF INVENTION: METHODS OF MODULATING APOPTOSIS
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSER: Burns, Doane, Swecker & Mathis
STREET: 699 Prince Street
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIATE: VA
COUNTRY: USA
ZIATE: Patanla PROMM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              844 AAGACCATGGACAAAGCCCTGGAGAAATCCAAAAAAGAGAGG 885
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Patent No. 6143522
GENERAL INFORMATION:
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US-09-499-082-9
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                                                                                                                                                                                                                                     310 CGGCAGGTGGACAGCCACGTGGAGCTGTTCGAGGCGCAGCAGGAGCTGGGCGACACAGTG 429
                                                                                               116 ArgGlnMetGluLeuHisSerGlnCysPheGlnAspProAlaGlu------- 130
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                            184 LysSerAlaLysLysLysArgSerLysAlaLysGlnGluArgGluAlaSerProVal
                                                                          76 LeuAsnGlnLysLysArgLeuGlnGlnLeuLeuGlnArgAlaLeuIleAsnSerGlnGlu
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       56 TyrGlnGluThrLeuLysGluIleAspAspValTyrGluLysTyrLysLysGluAspAsp
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TITLE OF INVENTION: METHOD OF MODULATING P53 ACTIVITY
FILLE REPERENCE: 02872-181
CURRENT APPLICATION NUMBER: US/09/159,871A
CURRENT FILING DATE: 1998-09-24
PRIOR APPLICATION NUMBER: US 60/060,138
PRIOR FILING DATE: 1997-09-26
PRIOR FILING DATE: 1998-01-14
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US-09-159-871-1
Sequence 1, Application US/09159871A; Patent No. 6420136; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PatentIn Ver. 2.0
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LOCATION: (16)..(897)
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SEQ ID NO 1
LENGTH: 2061
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                                                                                                                         244 SerieuThrTyrLysProLysGlyLysTrpTyrCysProLysCysArgGlyAspAsnGlu 263
                                                         243
                                                                                                                                                784 GGGCTCAATCATAAAACCCAAGGGCAAGTGGTACTGTCCCCAAGTGCCGGGGGGGAGAACGAG 843
GluMetIleGlyCysAspAsnGluGlnCysProIleGluTrpPheHisPheSerCysVal
                                                                                                                                                                                            264 LysThrMetAspLysSerThrGluLysThrLysLysAspArg 277
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ZIP: 22313-1404

CMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATR:
APPLICATION NUMBER: US/09/258,372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length:
Matches:
Conservative:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-513-365A-1 (1-280) x US-09-258-372-9 (1-2061)
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Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: Burns, Doane, Swecker & Mathis STREET: 699 Prince Street STREE: VA
                                                                                                                                                                                                                                                                                               Sequence 9, Application US/09258372
Patent No. 6238918
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Riabowol, Karl
TITLE OF INVENTION: SUPPRESSOR GENE INGI
TUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 028722-144
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-854-7400
TELEPHONE: 415-854-8275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/751,230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY AGENT INFORMATION:
NAME: Mooi, Leslie A.
REGISTRATION NUMBER: 37,047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 415-854-8275
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
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58.12%
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STRANDEDNESS: double
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Best Local Similari
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; LOCATION:
US-09-258-372-9
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Pred. No.:
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Search completed: January 12, 2004, 19:49:53 Job time : 84 secs

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Copyright (c) 1993 - 2004 Compugen Ltd.
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January 12, 2004, 17:22:12; Search time 430 Seconds (without alignments) 8721.912 Million cell updates/sec

Title: Perfect score:

US-09-513-365A-2 1080 Sequence:

IDENTITY_NUC Gapop 10.0 , Gapext 1.0 Scoring table:

2276164 seqs, 1736306516 residues Searched:

4552328 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

m2_6/ptodate/2/pubpna/PCT_NEW_PUB.seq:*
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m12_6/ptodate/2/pubpna/US07_NEW_PUB.seq:*
m12_6/ptodate/2/pubpna/US07_NEW_PUB.seq:*
m2_6/ptodate/2/pubpna/NS07_NEW_PUB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Sequence 7, Appli	Sequence 6, Appli	Sequence 37033, A	Sequence 4, Appli	Sequence 3454, Ap		9	Sequence 435, App	Sequence 435, App	Sequence 146, App	Sequence 146, App	Sequence 146, App	Sequence 257, App	Sequence 1178, Ap	Sequence 12517, A
SUMMAKIES	ΩI	US-10-115-899-7	US-10-115-899-6	US-09-918-995-37033	US-09-968-653A-4	US-09-764-877-3454	US-09-968-653A-2	US-09-968-653A-6	US-10-117-722-435	US-10-037-270-435	US-09-738-973-146	US-09-854-133-146	US-10-144-649A-146	US-09-801-368-257	US-09-938-842A-1178	US-09-908-975-12517
	DB	14	14	11	11	10	11	11	13	15	10	10	15	10	10	13
	Query Match Length DB	1078	840	421	873	8487	2061	633	1864	1864	451	451	451	993	813	9
æ	Query	96.9	77.6	35.0	22.0	17.0	16.9	16.1	8.5	. 8.5	7.7	7.7	7.7	6.2	5.7	2.6
	Score	1046	838.4	378.4	237.4	183.4	182.2	174.4	91.6	91.6	83.6	83.6	83.6	9.99	62	9
	Result No.	-	7	m	4	S.	9	7	80	6	10	11	12	13	14	15

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Gaps

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Indels

0; Mismatches

Best Local Similarity 99.5 Matches 1049; Conservative

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Query Match

96.9%; Score 1046; DB 14; Length 1078; 99.5%; Pred. No. 4.5e-240;

Sequence 23744, A	Sequence 16047, A	Sequence 6348, Ap	Sequence 5815, Ap			Sequence 4582, Ap	114	Sequence 2, Appli	521		262,		Sequence 12673, A		1502,	6502		502,	5502		14	86.	70	Sequence 90, Appl	48	-	49	Sequence 7, Appli	2
US-09-908-975-23744	US-09-918-995-16047	US-10-032-585-6348	US-09-814-353-5815	US-09-814-353-12097	US-09-814-353-18240	US-09-960-352-4582	US-09-919-580-114	ns	US-09-814-353-5212	US-09-814-353-11499	US-09-871-161-262	US-10-311-455-298	US-09-960-352-12673	US-10-128-714-2502	US-10-128-714-1502	US-10-128-714-6502	US-10-128-714-7502	US-10-128-714-502	US-10-128-714-5502	US-10-001-887-43	US-10-240-452-14	US-10-106-698-863	US-10-240-453-100	US-10-239-676-90	US-10-311-455-486	US-10-312-841-1		US-10-311-455-7	US-10-311-455-227
13			13			10	10	13	13												13				13	13	15	13	13
65	456	897	249	249	350	393	361	3673778	495	495	593	6071	277	912	1254	1254	1254	3254	3254	5520	6314	527	5689	5689	8805	3673778	624	18011	18154
5.4	5.3	5.0	4.9	4.9	4.8	4.8	4.7	4.6	4.6	4.6	4.5	4.5	4.5	4.5	4.5	4.5	4.5	4.5	4.5	4.5	4.5	4.4	4.4	4.4	4.4	4.4	4.4	4.4	4.3
58.6	56.8	54	52.8	52.8	51.6	51.6	50.8	49.6	49.2	49.2	49	49	48.8	48.6	48.6	48.6	48.6	48.6	48.6	48.4	48.4	48	47.6	47.6	47.6	47.6	47.2	47	46.8
16	11	18	19	20	21	22	23	24	25	56	27	28	53	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45
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ALIGNMENTS

Sequence 7, Application US/10115899;
Sequence 7, Application US/10115899;
Publication No. US20020151025A1
GENERAL INPORMATION:
FURLERAL INPORMATION:
FILE PEPERENCE: Q60193
CURRENT APPLICATION HUMBER: US/10/115,899
CURRENT FILING DATE: 2002-04-05
PRIOR APPLICATION NUMBER: 09/601,478
PRIOR FILING DATE: 1998-04-28
PRIOR FILING DATE: 1998-04-28 OTHER INFORMATION: human embryonic brain cDNA library TYPE: DNA ORGANISM: Homo sapiens ; NAME/KEY: CDS ; LOCATION: (92)..(931) US-10-115-899-7 LENGTH: 1078

엄 ð 셤 ò 셤 ò 엄 ઠે 8 ઠે a ò 셤 ٥. g ò 셤 ò 셤 ò g ઠે g ò 요 ò 셤 8 윱 ò 셤 ð

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      181 AAGGAAATTGATGATGTCTACGAAAAATATAAGAAAGAAGATGATTTAAACCAGAAGAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       241 CGTCTACAGCAGCTTCTCCAGAGAGCACTAATTAATAGTCAAGAATTGGGAGATGAAAAA
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                                                                                                                                                                                                                                                                                                                                                                                                     840;
GENERAL INFORWATION:

APPLICAMY: OSELUA Pharmaceutical Co., Ltd.

TITLE OF INVENTION: Human TSC403 gene and human INGIL gene
FILE REFERENCE: 060193
CURRENT APPLICATION NUMBER: US/10/115,899
CURRENT APPLICATION NUMBER: 09/601,478
FRIOR APPLICATION NUMBER: 09/601,478
PRIOR FILING DATE: 2000-08-03
PRIOR PLILING DATE: 1998-04-08
PRIOR PRILICE DATE: 1998-04-08
PRIOR PRILICE DATE: 1998-01-05
PRIOR PLILING DATE: 1998-01-05
PRIOR PLILING DATE: 1998-02-03
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      68 ATGTTAGGGCAGCAGCAGCAGCAACTGTACTCGTCGGCTGCGCTCC
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US-10-115-899-6
                                                                                                                                                                                                                                                                                                                                                                                                     14;
                                                                                                                                                                                                                                                                                                                                                                                                  77.6%; Score 838.4; DB 14;
99.9%; Pred. No. 2e-190;
iive 0; Mismatches 1;
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Best Local Similarity 99.9'
Matches 839; Conservative
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RESULT 2 US-10-115-899-6 Sequence 6, Application US/10115899 ; Publication No. US20020151025A1

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Publication No. US20030073084A1
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Pred. No. 1.8e-80;
0; Mismatches 26; Indels 0;
                                                                                                                                                                                                                                                                                        APPLICANT: Hyseq, Inc.
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
TITLE OF INVENTION: FROW VARIOUS CDNA LIBRARIES
FILE REFERENCE: 20411-76
CURRENT APPLICATION NUMBER: US/09/918, 995
CURRENT FILING DATE: 1090-01-30
PRIOR PELING DATE: 1990-01-20
NUMBER OF SEQ ID NOS: 38054
SOFWARE: FREESEQ for Windows Version 3.0
                                                                                                                                                                                                                                       Sequence 37033, Application US/09918995
Publication No. US20030073623A1
GENERAL INFORMATION:
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OTHER INFORMATION: n = A, T, C or G
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LOCATION: (1)...(421)
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LENGTH: 421
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Best Local Simi
Matches 394;
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RESULT 4 US-09-968-653A-4 ; Sequence 4, Application US/09968653A

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                                                   Garkavstev, Igor
Riabowol, Karl
TITLE OF INVENTION: p33/ING1 as a Mediator of p53 Signaling
Pathway
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                                                                                                                                                                                                        Boehnen Hulbert & Berghoff
                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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NAME: No. US20030073084Alnan, Kevin
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PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/09/006,783A
FILING DATE: 15-JAN-1998
                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 97,837
                                                                                                                                                                                                                          STREET: 300 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCATION: 7..813
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-913-0001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 873 base pairs
TYPE: nucleic acid
                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: McDonnell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 312-913-0002
GENERAL INFORMATION:
APPLICANT: Gudkov, Andrey
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59.0%;
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SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                            ZIP: 60606
COMPUTER READABLE FORM:
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Best Local Similarity 59.0
Matches 462; Conservative
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                                                                                                                                                                                                                                                  CITY: Chicago
STATE: Illinois
                                                                                                                                                     NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                        COUNTRY: USA
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5529 CCCAACAAG-CGCTCACGGCGGCAGCGCAACAACAACAACAGAACGTGAGAACGCGTCCAG
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                    ----CTGCTGAAAGTGAACGAGCCTCAGATAAAGCAAAGATGGATTCCAGCCAACCAGA
                                                                                                                                                                             565 GGCAAATGGGATTGAAGACTGTGATGATCAGCCACCTAAAGAAAAGAAATCCAAGTCAGC
                                                                                                                                                                                                         5648 CAAGAAGAAGAAGCGCTCCAAGGCCAAGGCGGAGGGGAGAGGCGTCCCCTGCCGACTCCC
                                                                                                                                                                                                                                                                                                                                                                                                                   745 AGGATGTGACAATGAACAGTGTCCAATTGAATGGTTTCACTTTTCATGTGTTTCACTTAC
                                                       6469 AACAGCGGCAAAGGCTGGCGCGGACAAGGCGAAGGCGAGCGCAGCGCAAGGCAAG
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                                                                                                                                                                                                                                                           625 AAAGAAAAAGAAACGCTCCAAGGCCAAGCAGGAAAGGGAAGCTTCACCTGTTGAGTTTGC
                                                                                                                                                                                                                                                                                                                                       685 ANTAGATCCTAATGAACCTACATACTGCTTATGCAACCAAGTGTCTTATGGGGAGATGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Garkavstev, Igor
Riabowol, Karl
TITLE OF INVENTION: p33/ING1 as a Mediator of p53 Signaling
Pathway
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/968,653A
FILING DATE: US/09/968,653A
FILING DATE: UD-OCt-2001
CLASSIFICATION: UDATA:
APPLICATION NUMBER: US/09/006,783A
FILING DATE: 15-JAN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Boehnen Hulbert & Berghoff
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NAME: No. US20030073084Alnan, Kevin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 97,837 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: McDonnell Boehnen Hu
STREET: 300 South Wacker Drive
CITY: Chicago
STATE: 11linois
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REGISTRATION NUMBER: 35,303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2, Application US/09968653A Publication No. US2003003084A1 GENERAL INFORMATION: Gudkov, Andrey V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: 312-913-0001
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INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
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US-09-968-653A-2
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GGCGCAGCAGGAGCTGGGCGACACAGTGGGCAACAGCGCAAGGTTGGCCGCGGACAGGCC
                                                                                                                                                                                                 595 GCCACCTAAAGAAAAGAAATCCAAGTCAGCAAAGAAAAAGAAACGCTCCAAGGCCAAGCA
                                                                                                                                                                                                                          648 GTGCAACCAGGTCTCCTATGGGGAGATGATCGGCTGCGACAACGACGAGTGCCCCATCGA
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                                     477 AAGCAAAGATGGATTCCAGCCAACCAGAAAGATCTTCAAGAAGACCCCGCAG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REPERBNCE: PC005
CURRENT RILIAG DATE: 2001-01-17
Prior application data removed - refer to PALM or file wrapper
NUMBER OF SEQ ID NOS: 4031
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Pred. No. 5.5e-33;
0; Mismatches 266;
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US-09-764-877-3454
; Sequence 3454, Application US/09764877
; Patent No. US20020147140A1
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57.0%;
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Best Local Similarity 57.0
Matches 395; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-877-3454
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GAG 830
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LENGTH: 8487
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522 CCCGCAGGCAGCGGACCAGTGAAAGCCGTGATTTATGTCACATGGCAAATGGGATTGAAG 581
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        422 CCACGTACTGTCTGTGCAACCAGGTCTCCTATGGGGAGATGATCGGCTGCGACAACGACG 481
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                                                                                                                   Berghoff
                                                                                                                                                                                                                                                                                        ZIP: 60606
COMPUTER READMBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 11;
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Pred. No. 1.6e-31;
0; Mismatches 126;
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                                                                                                            ADDRESSEE: McDonnell Boehnen Hulbert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: NO. US20030073084Alnan, Kevin
REGISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 97,837
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
APPLICATION UNMERS: US/09/968,653A
FILING DATE: 01-0ct-2001
CLASSIFICATION: <unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION UNMBER: US/09/006,783A
FILING DATE: 15-JAN-1998
ATTORNEY/AGENT INFORMATION:
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SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-968-653A-6
                                                                                                                                                     STREET: 300 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 633 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: 312-913-0001
           Pathway
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 312-913-0002 INFORMATION FOR SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        602 AATCCAAAAAAGAGAG 617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           882 AGACAAAAAAGGATAG 897
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 66.5%;
Matches 250; Conservative
                                            NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: cDNA
                                                                                                                                                                                   CITY: Chicago
STATE: Illinois
                                                                                                                                                                                                                                                             COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           642
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          314 GCGACGAGAAGATCCAGATCGTGAGCCAGATGGTGGAGCTGGTGGAGAGCTGGAGAACCGCACGCGGC 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                374 Aggrácia con contra de contra de
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     434 ACAGCGGCAAGGTTGGCGCGGACAGGCCCAATGGCGATGCGGTAGCGCAGTCTGACAAGC 493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            509 TCTTCAAGAA--GACCCCGCAGGCAGCGACCAGTGAAAGCCGTGATTTATGTCACATGG 566
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CCAACAGCAAGCGCTCACGGCGGCAGCGCAACAACAAGAACCGTGAGAACGCGTCCAGCA 553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          626
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                554 ACCACGACCACGACGCCCTCGGGCACACCCAAGGAGAAGAAGAAGGAGGCCAAGACCTCCA 613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 627 AGAAAAAGAAACGCTCCAAGGCCAAGCAAAAGGAAAGCTTCACCTGTTGAGTTTGCAA 686
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AGAAGAAGAAGCGCTCCAAGGCCAAGGCGAGCGAGGGCGTCCCCTGCCGACCTCCCCA 673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TAGATCCTAATGAACCTACATACTGCTTATGCAACCAAGTGTCTTATGGGGAGATGATAG 746
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TGBACCCCAACGAACCCACGTACTGTGCAACCAGGTCTCCTATGGGGAGATGATCG 733
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GATGTGACAATGAACAGTGTCCAATTGAATGGTTTCACTTTTCATGTGTTTCACTTACCT 806
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  853
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   567 CAAATGGGATTGAAGACTGTGATGATCAGCCACCTAAAGAAAAGAAATCCAAGTCAGCAA
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Riabowol, Karl
TITLE OF INVENTION: p33/ING1 as a Mediator of p53 Signaling
                                                                                                                                                                                                                                                                                                                                                                                                           DB 11; Length 2061;
                                                                                                                                                                                                                                                                                                                                                                                            Query Match
16.9%; Score 182.2; DB 11; Length
Best Local Similarity 56.9%; Pred. No. 4.5e-33;
Matches 393; Conservative 0; Mismatches 268; Indels
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                                                                                                                                                                                                                                   ; SEQUENCE DESCRIPTION: SEQ ID NO: US-09-968-653A-2
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LENGTH: 2061 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Gudkov, Andrey V
                                                                                                            TOPOLOGY: linear
                                                                                                                                             MOLECULE TYPE: cDNA FEATURE:
                                                                                                                                                                                                                    NAME/KEY:
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1274 gérgagárdergegartergáraaccaagarrecceraragaartegriccarrarescriée 1333
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              674 GITGAGITIGCAAIAGAICCIAAIGAACCIACAIACIGCITAIGCAACCAAGIGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8.5%; Score 91.6; DB 15; Length 1864; 64.8%; Pred. No. 2.1e-11;
                                                   APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: No. US20030104529Alel Nucleic Acids and
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 784CIP2B
CURRENT APPLICATION NUMBER: US/10/037,270
CURRENT FILING DATE: 2002-01-04
PRIOR PRIOR PILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: 09/552,317
PRIOR FILING DATE: 2000-01-21
PRIOR FILING DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 1104
SOSTWARE: pt_FL_Genes Version 1.0
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APPLICANT: Kalos, Michael D.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: THE THERAPY AND DIAGNOSIS OF LUNG CANCER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  734 GGGGAGATGATAGGATGTGACAATGAACAGTGTCCAATTGAATGGTT
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CURRENT APPLICATION NUMBER: US/09/738,973
CURRENT FILING DATE: 2000-12-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Sequence 146, Application US/09738973
; Patent No. US20020110563A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Henderson, Robert J
Lodes, Michael J.
Fling, Steven P.
Mohamath, Raodoh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Algate, Paul A.
Secrist, Heather
Indirias, Carol Yo
Benson, Darin R.
Elliot, Mark
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 64.8
Matches 136; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Reed, Steven G.
Wang, Zniwer
Tillinghast,
                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: CDS
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                                                                                                                                                                                                                                                                                                                                                                      SEQ ID NO 435 LENGTH: 1864
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1274 GGTGAGATGGTGGGATGTGATAACCAAGATTGCCCTATAGAATGGTTCCATTATGGCTGC 1333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1334 Griggarigacagaggcaccaaaaggcaaarggracigiccacagrgcacrgcracaarg 1393
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     794 GITICACITACCIATAAACCAAAGGGGAAATGGTATTGCCCAAAGTGCAGGGGAGATAAT 853
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              674 GTTGAGTTTGCAATAGATCCTAATGAACCTACATACTGCTTATGCAACCAAGTGTCTTAT
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                                                                                                                                                 APPLICANT: Tang, Y. Tom
APPLICANT: Liu, Chenghua
APPLICANT: Liu, Chenghua
APPLICANT: Asundi, Vinod
APPLICANT: Asundi, Vinod
APPLICANT: Asundi, Vinod
APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: No. US20030219744A1e1 Nucleic Acids and
TITLE OF INVENTION: No. US2003021974A1e1 Nucleic Acids and
TITLE OF INVENTION: No. US2003021974A1e1 Nucleic Acids and
TITLE OF INVENTION: NUMBER: US/10/117,722
CURRENT APPLICATION NUMBER: US/02-04-04
PRIOR APPLICATION NUMBER: 09/620,312
PRIOR PILING DATE: 2000-07-19
PRIOR FILING DATE: 2000-01-21
PRIOR FILING DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 1104
SOFTWARE: PL genes Version 1.0
SEQ ID NO 435
LENGTH: 1864
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Pred. No. 2.1e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1394 AAGAGAAGAGCAGCAGACACAAATAAAGG 1423
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5. US20030104529A1
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Best Local Similarity 64.8%;
Matches 136; Conservative
                                                                                                              US20030219744A1
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APPLICANT: Liu, Chenghua
APPLICANT: Asundi, Vinod
APPLICANT: Zhang, Jie
APPLICANT: Ren, Feiyan
APPLICANT: Chen, Rulhong
APPLICANT: Zhao, Qing A.
APPLICANT: Wehrman, Tom
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Jian-Rui
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Wang, Dunrui
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; LOCATION: (164)..(1420)
US-10-117-722-435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
ORGANISM: Homo sapiens
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US-10-144-649A-146
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APPLICANT:
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                                                                                                                                         GAAATACCAAGAATCCTGAAGGAGCTAGACGAGTGCTACGAGCGCTTCAGTCGCGAGAC 135
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                                                                                                        CATCGAGTCCCTGCCTTTCGACTTGCAGAAATGTCTCGCTGATGCGGGAGATCGACGC 75
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APPLICANT: Henderson, Robert A.
APPLICANT: Henderson, Robert A.
APPLICANT: Benson, Darin R.
APPLICANT: Benson, Darin R.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: THE THERAPY AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121 475C10
CURRENT APPLICATION NUMBER: US/09/854,133
CURRENT FILING DATE: 2001-05-11
NUMBER OF SEQ ID NOS: 735
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 146
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   Length 451;
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0; Mismatches 114;
                                   0; Mismatches 114;
Score 83.6; DB 10;
Pred. No. 7.3e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 146, Application US/09854133 Publication No. US20020183499A1 GENERAL INFORMATION: APPLICANT: Lodes, Michael J.
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7.7%;
58.6%;
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Best Local Similarity 58.6
Matches 163; Conservative
                                   Conservative
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ORGANISM: Homo sapien
                Similarity
Query Match
Best Local Simi
Matches 163;
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IITLE OF INVENTION: Methods for Improving Secondary Metabolite Production in Fungi
FILE REFERENCE: 109272.147
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Sequence 146, Application US/10144649A
| Publication No. US2030118599A1
| GENERAL INFORMATION:
| APPLICANT: Lodges, Michael J.
| APPLICANT: Mang, Tongtong
| APPLICANT: Fan, Liqun
| APPLICANT: Algate, Paul A.
| APPLICANT: McNeill, Patricia D.
| TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TITLE OF INVENTION: COMPOSITIONS AND DIAGNOSIS OF LUNG CANCER FILE REFERENCE: 210121.475C11
| CURRENT PELLING DATE: 2002-08-21
| NUMBER OF SEQ ID NOS: 749
| SOCTWARE: FatlSEQ for Windows Version 3.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches 114;
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Pred. No. 7.3e-10;
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CURRENT FILING DATE: 2001-03-07
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PRIOR FILING DATE: 2000-01-19
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US-09-801-368-257
; Sequence 257, Application US/09801368
; Patent No. US20020128250A1
; GENERAL INFORMATION:
; APPLICANT: Busby, Robert
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No. US20020128250Alman,
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Holtzman, Doug
Madden, Kevin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 58.6
Matches 163; Conservative
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Silva, Jeff
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Cali, Brian
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ORGANISM: Homo sapien
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              729 CTTATGGGGAGATGATAGGATGTGACAATGAACAGTGTC---CAATTGAATGGTTTCACT 785
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      895 gcagacrigigagciagaarggirccarrigccargrariggacricgaaacrcraccraag 954
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              662 atacatécerregecercacacergagaceagarreaaagggaaarg 707
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Pred. No. 0.00016;
0; Mismatches 55;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              955 GGCAAGTGGTATTGCGACGACTGCA 979
PRIOR APPLICATION NUMBER: US 60/160,587
PRIOR FILING DATE: 1999-10-20
NUMBER OF SEQ ID NOS: 440
SEQ ID NO 257
LENGTH: 993
                                                                                                                                                                                                                                                                                                                  ; ORGANISM: Saccharomyces cerevisiae US-09-801-368-257
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; ORGANISM: Arabidopeis thaliana
US-09-918-842A-1178
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Best Local Similarity 65.1%;
Matches 108; Conservative
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US-09-908-975-12517
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GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

January 12, 2004, 16:38:42 ; Search time 93 Seconds (without alignments) 5125.740 Million cell updates/sec Run on:

Title: Perfect score:

Sequence:

IDENTITY_NUC Gapop 10.0 , Gapext 1.0 Scoring table:

569978 seqs, 220691566 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

1: /cgn2_6/ptodata/2/ina/5A COMB.seq:*
2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/PCTUS COMB.seq:*
6: /cgn2_6/ptodata/2/ina/PcTUS COMB.seq:* Issued Patents NA: Database:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

			ď			SUMMARIES	
Result No.		Score	Query Match	° Query Match Length	DB	ID	Description
	1 1	1046	96.9	1078	4	US-09-601-478-7	Sequence 7, Appli
	2 83	838.4	77.6	840	4	US-09-601-478-6	ω.
	3 825	2.5	76.4	1154	4	US-09-484-970B-81	Sequence 81, Appl
	4 23	237.4	22.0	873	٣	US-09-006-783A-4	4
	5 18	183.8	17.0	1902	7	US-09-258-257-1	1
	6 183	13.8	17.0	1902	~	US-09-258-371-1	٦,
	7 18	183.8	17.0	1902	ო	US-08-569-721A-1	7
	8 18	183.8	17.0	1902	m	US-08-751-230-1	-
	9 18	183.8	17.0	1902	m	US-09-499-082-1	Sequence 1, Appli
_	10 18	183.8	17.0	1902	m	US-09-258-372-1	٦,
•-7	11 18	183.8	17.0	2061	~	US-09-258-371-9	6
* 1	12 18	183.8	17.0	2061	m	US-08-751-230-9	Sequence 9, Appli
-	13 18	183.8	17.0	2061	٣	US-09-499-082-9	6
-7	14 18	183.8	17.0	2061	m	US-09-258-372-9	Sequence 9, Appli
-	15 18	182.2	16.9	2061	ო	US-09-006-783A-2	~
-	16 18	182.2	16.9	2061	4	US-09-159-871-1	-
	_	174.4	16,1	633	m	US-09-006-783A-6	9
		92.6	8.9	678	m	US-09-195-286-3	'n
-	6 61	9.5	8.9	669	ო	US-09-195-286-2	Sequence 2, Appli
• •		1.6	8.5	1864	4	US-09-620-312D-435	435
• •		83.6	7.7	451	4	US-09-370-838-146	146,
O	22 7	72.4	6.7	7218	Н	US-08-232-463-14	14, A
. •	23	20.6	4.7	860	н	US-07-847-010-18	18,
U	. 4	49	4.5	593	ო	US-09-385-982-262	262,
	25 4	8.9	4.3	6124	4	US-08-213-419B-3	3, A
. 1	26 4	6.2	4.3	1189	-	US-07-781-034-4	4
. 4	27 4	6.2	4.3	1189	Ŋ	PCT-US92-08328-4	4

Sequence 13, Appl	Sequence 1, Appli	Sequence 20, Appl	Sequence 20, Appl	Sequence 20, Appl	Sequence 1, Appli	Sequence 3, Appli	Sequence 124, App	Sequence 89, Appl	Sequence 3, Appli	Sequence 251, App	Sequence 12, Appl	Sequence 11, Appl	Patent No. 5198345				
US-08-487-826B-13	US-08-916-421B-1	US-09-852-067-1	US-08-728-323A-1	US-09-298-568-1	US-09-410-399-1	US-08-770-379-20	US-08-757-669A-20	US-09-230-371A-20	US-08-665-716-1	US-09-208-742-3	US-09-489-847-124	US-09-489-847-89	US-09-130-491-3	US-09-385-982-251	US-08-956-307B-12	US-08-956-307B-11	5198345-16
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45.8	45.8	43.8	43.8	43.8	43.8	43.8	43.8	43.8	43.4	43.2	43	43	43	42.8	42.8	42.8	42.8
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US-09-601-478-7

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61 CGGCAGGATGTTAGGGCAGCAGCAGCAGCAACTGTACTCGTCGGCTGCGCTCCTGACCGG 120
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Sequence 7, Application US/09601478

Patent No. 6403785

GENERAL INFORMATION:

APPLICANT: Ostuka Pharmaceutical Co., Ltd.

TITLE OF INVENTION:

FILE REPERENCE: Q60193

CURRENT PELLING DATE: 2000-03

PRIOR APPLICATION NUMBER: UF H10-134679

FRIOR FILING DATE: 1998-04-28

PRIOR FILING DATE: 1998-03-05

PRIOR FILING DATE: 1998-03-05

PRIOR FILING DATE: 1998-03-05

PRIOR RILING DATE: 1998-03-05

PRIOR RILING DATE: 1998-02-03

NUMBER OF SEQ ID NOS: 11

SOFTWARE: Patentin Ver: 2.1.

SEQ ID NOS: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              96.9%; Score 1046; DB 4; Length 1078; 99.5%; Pred. No. 4.4e-264; Live 0; Mismatches 5; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: human embryonic brain cDNA library NAME/KEY: CDS LOCATION: (92)..(931)
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Matches 1049; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 1078
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Length 840; Indels 120 247 180 307

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                                                         FEATURE: OTHER INFORMATION: human embryonic brain cDNA library
                                                                                                           Score 838.4; DB 4;
Pred. No. 7.9e-210;
0; Mismatches 1;
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Patent No. 6426186
                                                                                                            77.6%;
                                                                                                                        Best Local Similarity 99.9
Matches 839; Conservative
                  LENGTH: 840
TYPE: DNA
ORGANISM: Homo sapiens
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US-09-484-970B-81
SEQ ID NO 6
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CURRENT APPLICATION Human TSC403 gene and har FILE REFERENCE: 060193
CURRENT APPLICATION NUMBER: US/09/601,478
CURRENT FILING DATE: 1908-003
PRIOR APPLICATION NUMBER: JP H10-134679
PRIOR PILING DATE: 1998-03-05
PRIOR APPLICATION NUMBER: JP H10-3234
PRIOR PILING DATE: 1998-03-05
PRIOR PILING DATE: 1998-02-03
PRIOR FILING DATE: 1998-02-03
PRIOR FILING DATE: 1998-02-03
PRIOR FILING DATE: 1998-02-03
PRIOR FILING DATE: 1998-02-03
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gene and l
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      265 CTACGAAAAATATAAGAAAGAAGATGATTTAAACCAGAAGAAACGTCTACAGCAGCTTCT 324
                                                                                         1021 AAGGGTTATTTGTCTTTTATATTCGTTTGCTTTCAGAAAAGGTTTTAGGGTAAATGC
                                                                                                                                                  ATAAGACTATGCAATAATTTTTAATCATTAGTATTAATGGTGTATTAAAAGTTGTTGTAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Garkavstev, Igor
TITLE OF INVENTION: p33/ING1 as a Mediator of p53 Signaling
TITLE OF INVENTION: Pathway
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS: ADDRESSE: ADD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 873;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FPILING NUMBER: US/09/006,783A
FILING DATE: 15-JAN-1998
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 3;
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Pred. No. 1.4e-52;
0; Mismatches 291;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 4, Application US/09006783A Patent No. 6297366 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: No. 6297366nan, Kevin
REGISTRATION NUMBER: 35,303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 97
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-913-0001
                                                                                                                                                                                                                                                                      TTTGAAAAAAAAA 1064
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59.0%;
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INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 873 base pairs
TYPE: nucleic acid
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Best Local Similarity 59.0
Matches 462; Conservative
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; LOCATION:
US-09-006-783A-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TGCTGAAAGTGAACCCACAGATAAAGCAAAGATGCATTCCAGCCAACCAGAAAGATC
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Pred. No. 2.7e-206;
                       APPLICANT: Jones, Karen A.
APPLICANT: Volkmuth, Wayne
APPLICANT: Walker, Wichael G.
TITLE OF INVENTION: BONE REMODELING GENES
FILE REFERENCE: PB-0014 US
CURRENT APPLICATION NUMBER: US/09/484,970B
CURRENT FILING DATE: 2000-01-18
NUMBER OF SEQ ID NOS: 172
SOFTWARE: PERL Program
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Best Local Similarity 97.9%;
Matches 836; Conservative
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US-09-484-970B-81
GENERAL INFORMATION:
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LOCATION: 17-37
                                                                                                                                                                                                                                                                            SEQ ID NO 81
LENGTH: 1154
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57.0%; Pred. No. 2.2e-38;
tive 0; Mismatches 267;
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              PRICE APPLICATION DATA:
APPLICATION NUMBER: US 08/569,721
FILING DATE: 08-DEC-1995
ATTOCNEY AGENT INFORMATION:
NAME: MOOI, Leslie A.
REGISTRATION NUMBER: 37,047
REFECCOMMINICATION INFORMATION:
TELECOMMINICATION: (650) 854-7400
                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 1 SEQUENCE CHARACTERISTICS: LENGTH: 1902 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 57.0
Matches 394; Conservative
                                                                                                                                                                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: single
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109..738
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LOCATION:
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                                                              CCAGAGAGCACTAATTAATAGTCAAGAATTGGGAGATGAAAAAATACAGATTGTTACACA
                                                                                                   228 GCAGCGCGCCTGATCCGCAGCCAGGAGCTGGGCGACGAGAAGATCCAGATCGTGAGCCA
                                                                                                                                            AATGCTCGAATTGGTGGAAAATCGGGCAAGACAAATGGAGTTACACTCACAGTGTTTCCA
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APPLICANT: RIABOWOL, Karl
TITLE OF INVENTION: DNA SEQUENCE ENCODING A TUMOR
TITLE OF INVENTION: SUPPRESSOR GENE
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
APPLICATION NUMBER: US/09/258,257
FILING DATE:
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CITY: Alexandria
STATE: Virginia
COUNTRY: United States
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Patent No. 5965398
GENERAL INFORMATION:
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                                                                  509 TCTTCAAGAA--GACCCCGCAGGCAGCGGACCAGTGAAAGCCGTGATTTATGTCACATGG 566
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   275 ACAGCGGCAAGGTTGGCGCGGACAGGCCCAATGGCGATGCGGTAGCGCAGTCTGACAAGC 334
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APPLICATION NUMBER: US/08/569,721A FILING DATE: 08-DEC-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: P.O. Box 1404
CITY: Alexandria STREE: Virginia
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COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1, Application US/08569721A; Patent No. 6037121; GENERAL INFORMATION:
APPLICANT: GARKAVTSEV, IGOT
APPLICANT: RIABOWOL, Karl
TITLE OF INVENTION: DNA SEQUENCE ENV
TITLE OF INVENTION: SUPPRESSOR GENE
NUMBER OF SEQUENCES: 12
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FILING DATE: 08-DEC-1999
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: MOOJ, Leslie A.
REGISTRATION NUMBER: 37,047
REFERENCE/DOCKET NUMBER: 0287
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION: (550) 854-7400
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INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
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TYPE: nucleic acid
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ADDRESSEE: Burns, Do
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NAME/KEY: CDS
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US-08-569-721A-1
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                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Garkavtsev, Igor
APPLICANT: Riabowoll Karl
TITLE OF INVENTION: DNA SEQUENCE ENCODING THE TUMOR
TITLE OF INVENTION: SUPPRESSOR GENE ING1
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .2e-38
                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Burns, Doane, Swecker & Mathis STREET: 699 Prince Street
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 223113-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
695 ACAAAGCCCTGGAGAAATCCAAAAAAGAGAG 725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. 2.2e
; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   417 AAATGGAGTTACACTCACAGTGTTTCCAAGATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 183.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: MOOI, Leslie A. REGISTRATION NUMBER: 37,047
REFERENCE/DOCKET NUMBER: 028722-144
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-854-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/258,371
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/751,230
                                                                                                                                                   Sequence 1, Application US/09258371
Patent No. 5986078
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illarity 57.0%;
Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 1902 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 1902 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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Best Local Simi
Matches 394;
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US-09-258-371-1
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                                                                                   CMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: Patentin Release #1.0, Version #1.30
SUGNESST PERCHION Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/751,230
FILING DATE: 15-NOV-1996
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/569721
FILING DATE: 08-DEC-1995
ATTORNEY/AGENT INFORMATION:
NAME: MOOI, Leslie A.
REGISTRATION NUMBER: 37,047
REGISTRATION NUMBER: 37,047
REGISTRATION NUMBER: 37,047
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Pred. No. 2.2e-38;
0; Mismatches 267;
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-854-7400
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Best Local Similarity 57.0%;
Matches 394; Conservative (
                                                       Floppy disk
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MOLECULE TYPE: cDNA
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US-08-751-230-1
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                                                                                                                                                      Score 183.8; DB 3;
Pred. No. 2.2e-38;
0; Mismatches 267;
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699 Prince Street
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APPLICANT: Riabowol, Karl
TITLE OF INVENTION: SUPPRESSOR GENE INGI
TITLE OF INVENTION: SUPPRESSOR GENE INGI
NUMBER OF SEQUENCES: 23
CARRESPONDENCE ADDRESS:
ADDRESSEE: BURNE, Doane, Swecker & Mati
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; Sequence 1, Application US/08751230
; Patent No. 6117633
                                                                                                                                                      Query Match
Best Local Similarity 57.0%;
Matches 394; Conservative
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STATE: VA
COUNTRY: USA
ZIP: 22313-1404
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LOCATION:
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US-08-569-721A-1
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                                            95 cacadalacedecedarecretecarererererecedecedecedecedecededeceded
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STREET: 699 Prince Street
CITY: Alexandria
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Patent No. 6238918
GENERAL INFORMATION:
APPLICANT: Riabowol, Karl
TILLE OF INVENTION: DNA SEQUENCE ENCOD:
TITLE OF INVENTION: SUPPRESSOR GENE INVENTION: ORDERSOR GENE INVENTION: ADDRESS:
CORRESPONDENCE ADDRESS:
ADDRESSEB: BURNES:
STREET: 699 Prince Street
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, V
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/258,372
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CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/751,230
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ZIP: 22313-1404
COMPUTER READABLE FORM:
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US-09-258-372-1
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635 ATAAACCCAAGGGCAAGTGGTACTGTCCCAAGTGCCGGGGGGAAAAACGAAAAAACATGG
                                            807 ATAAACCAAAGGGGAAATGGTATTGCCCAAAGTGCAGGGGAGATAATGAGAAAACAATGG
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                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Helbing, Caren C.
APPLICANT: Riabowol, Karl
APPLICANT: Johnston, Randall N.
APPLICANT: Garkavtesov, Igor
ITILE OF INVENTION: METHODS OF MODULATING APPTOSIS
NUMBER OF SEQUENCES: 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/499,082
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches 267;
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T: 699 Prince Street
Alexandria
                                                                                                                                                                              ACAAAGCCCTGGAGAATCCAAAAAAGAGAG 725
                                                                                                                                      867 ACAAAAGTACTGAAAAGACAAAAAAGGATAG 897
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/828,158
FILING DATE: 27-MAR-1997
APPLICATION NUMBER: US 08/751230
FILING DATE: 15-NOV-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/569721
FILING DATE: 08-DEC-1995
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REGISTRATION NUMBER: 37,047
REFRENCE/DOCKET NUMBER: 0287;
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-854-9400
TELEFAX: 650-854-8275
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                            Sequence 1, Application US/09499082
Patent No. 6143522
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LENGTH: 1902 base pairs
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MEDIUM TYPE: Floppy
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STRANDEDNESS: double
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Best Local Similarity
Matches 394; Conserv
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US-09-499-082-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                297 ACCAGAAGAACGICTACAGCAGCTICTCCAGAGAGCACTAATTAATAGTCAAGAATTGG
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBW PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
APPLICATION NUMBER: US/09/258,371
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Pred. No. 2.3e-38;
0; Mismatches 267;
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                                                                           Sequence 9, Application US/09258371
Patent No. 5986078
GENERAL INPORMATION:
APPLICANT: Garkavtsev, Igor
APPLICANT: Riabowol, Karl
TITLE OF INVENTION: SUPPRESSOR GENE ING1
TITLE OF INVENTION: SUPPRESSOR GENE ING1
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis
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APPLICATION NUMBER: 08/751,230
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Mooi, Leslie A.
REGISTRATION NUMBER: 37,047
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-854-7400
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Best Local Similarity 57.0%;
Matches 394; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 2061 base pairs
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STRANDEDNESS: double
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US-09-258-371-9
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RESULT 11
US-09-258-371-9
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17.0%; Score 183.8; DB 3;
Best Local Similarity 57.0%; Pred. No. 2.2e-38;
Matches 394; Conservative 0; Mismatches 267;
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                                                                                                                                                                                                     028722-144
                                                                                           NAME: Mooi, Leslie A.
REGISTRATION NUMBER: 37,047
REFERENCE/DOCKET NUMBER: 02877
TELECOMMUNICATION INPORMATION:
TELEPAN: 415-854-7400
TELEPAX: 415-854-8275
INPORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:
                                             ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 1902 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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; LOCATION: 109
US-09-258-372-1
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                                                                                                                                                                  Gaps
                                                                                                                                                               30;
                                                                                                     Length 2061;
                                                                                                  Score 183.8; DB 3; Length;
Pred. No. 2.3e-38;
0; Mismatches 267; Indels
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APPLICANT: Helbing, Caren C.
APPLICANT: Halbing, Karl
APPLICANT: Rabowol, Karl
APPLICANT: Garkavtsev, Igor
TITLE OF INVENTION: METHODS OF MODULATING APOPTOSIS
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3: Burns, Doane, Swecker & Mathis 699 Prince Street
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Patent No. 6143522
                                                                                                  Query Match
Best Local Similarity 57.0%;
Matches 394; Conservative
            16..900
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STATE: VA
COUNTRY: USA
            LOCATION:
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US-08-751-230-9
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US-09-499-082-9
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                                                                                                                                                     554 ACCACGACCACGACGACGCCTCGGGCACACCCAAGGAGAAGAAGAAGACCTCCA
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                                                                                            567 CAAATGGGATTGAAGACTGTGATGATCAGCCACCTAAAGAAAAGAAATCCAAGTCAGCAA
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APPLICANT: Garkavtesv, Igor
APPLICANT: Riabowol, Karl
TITLE OF INVENTION: DNA SEQUENCE ENCODING THE TUMOR
TITLE OF INVENTION: SUPPRESSOR GENE ING!
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis
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APPLICATION NUMBER: US/08/751,230 FILING DATE: 15-NOV-1996
CLASSIFICATION: 514
PRICA APPLICATION DATA:
APPLICATION NUMBER: US 08/569721
FILING DATE: 08-DEC-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: 699 Prince Street
CITY: Alexandria
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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REGISTRATION NUMBER: 37,047
RELECOMMUNICATION INFORMATION:
TELEPHONE: 415-854-7400
TELEPHONE: 415-854-7400
INFORMATION FOR SEQ ID NO: 9: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 9, Application US/08751230 Patent No. 6117633
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STRANDEDNESS: double
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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MOLECULE TYPE: CDNA
FEATURE:
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687 TAGATCCTAATGAACCTACATACTGCTTATGCAACCAAGTGTCTTATGGGGAGATGATAG
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Pred. No. 2.3e-38;
0; Mismatches 267;
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STREET: 699 Prince Street
CITY: Alexandria
                                                                                                                                                                                                                                                                             854 ACAAAGCCCTGGAGAAATCCAAAAAAGAGAG 884
                                                                                                                                                                                                                                             867 ACAAAAGTACTGAAAAGACAAAAAAGGATAG 897
                                                                                                                                                                                                                                                                                                                                                                        Sequence 9, Application US/09258372
; Sequence 10. 6238918
; GENERAL INFORMATION:
    APPLICANT: Garkavtsev, Igor
    APPLICANT: Riabowol, Karl
    TITLE OF INVENTION: DNA SEQUENCE ENCODING:
    TITLE OF INVENTION: SUPPRESSOR GENE ING1
    NUMBER OF SEQUENCES: 23
    CORRESPONDENCE ADDRESS:
    ADDRESSEB: Burns, Doane, Swecker & Mathie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/258,372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
REDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/751,230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
ATTORNEY/AGENT:
NAME: Moci, Lealie A.
REGISTRATION NUMBER: 37,047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 02
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-854-7400
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57.0%;
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Best Local Similarity 57.03
Matches 394; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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STRANDEDNESS: double
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ZIP: 22313-1404
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; LOCATION:
US-09-258-372-9
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US-09-258-372-9
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                                                                                                   PatentIn Release #1.0, Version #1.30
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                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/828,158
APPLICATION NUMBER: US/08/828,158
APPLICATION NUMBER: US 08/751230
FILING DATE: 15-NOV-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/569721
FILING DATE: 08-DEC-1995
ATTORNEY/AGENT INFORMATION:
NAME: Mooi, Leslie A.
REGISTRATION NUMBER: 37,047
REJECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-854-7400
                                                                                                                      CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/499,082
FILING DATE:
CLASSIFICATION:
                         MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS COSTWARE: Patentin Poles
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57.0%;
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INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 57.03
Matches 394; Conservative
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STRANDEDNESS: double
  ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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; LOCATION:
US-09-499-082-9
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237 AAGAAACGTTAAAGGAAATTGAFGATGTCTACGAAAAATATAAGAAAGAAGATGATTTAA 296
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56.9%; Pred. No. 6.1e-38;
tive 0; Mismatches 268;
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NAME: No. 6297366nan, Kevin E
REGISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 97,837
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-913-0001
TELEFACENT 312-913-0002
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 2061 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                 97,837
                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 56.9
Matches 393; Conservative
                                                                                                                                                                                                                                                                                                                               16..897
                                                                                                                                                                                                                                                                 MOLECULE TYPE:
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LOCATION:
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                                            254 CGCAGAAGCGGCGGATGCTGCACTGTGCAGCGCGCGCTGATCCGCAGCCAGGAGCTGG
                                                                                       GAGATGAAAAATACAGATTGTTACACAAATGCTCGAATTGGTGGAAAATCGGGCAAGAC
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COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/006,783A

FILLNG DATE: 15-JAN-1998

CLASSIFICATION: 435
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Patent No. 6297366
GENERAL INFORMATION:
APPLICANT: Garkavstev, Igor
APPLICANT: Riabowol, Karl
TITLE OF INVENTION: Pathway
TITLE OF INVENTION: Pathway
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CORRESPONDENCE ADDRESS:
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CITY: Chicago
STATE: Illinois
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US-09-006-783A-2
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Copyright (c) 1993 - 2004 Compugen Ltd.		7	711	65.8	793	10	BE796780 ·	
		80	694.2	64.3	778	12	BI548536	
		σ	680.8	63.0	919	10	BG211544	
cleic search, using sw model	υ	10	671.8	62.2	675	12	BM682789	
		;	663	4 61	664	1,	DM719460	

OM nucleic - nucleic search, using sw model

Run on: January 12, 2004, 16:38:42; Search time 2229 Seconds (without alignments)

11776.058 Million cell updates/sec

Title: US-09-513-365A-2

Perfect score: 1080
Sequence: 1 gcggccggcgggcatg.....aaaaaaaaaaaaaaaaa 1080
Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0
Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : EST:*
1: em estba:*
2: em_esthum:*
3: em estin:*
4: em_estin:*
5: em estpl:*
7: em_estpl:*
7: em_estpl:*
10: gb_estl:*
10: gb_estl:*
11: gb_htc:*
12: gb_estl:*
13: gb_estl:*
14: gb_estl:*

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17: em_gss_hum.*

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19: em_gss_hum.*

20: em_gss_vrt.*

21: em_gss_vrt.*

22: em_gss_vrt.*

24: em_gss_mus.*

25: em_gss_mus.*

26: em_gss_pbg:*

27: em_gss_pbg:*

28: gb_gss2:*

29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	AKO48800 Mus muscu	AK083144 Mus muscu	AK012716 Mus muscu	BQ277444 AGENCOURT
SUMMARIES	ID	AK048800	AK083144	AK012716	BQ277444
	80	11	1	ij	13
	Query Match Length DB	2643	2812		
de	Query Match	828 76.7	9.92	75.3	69.5
	Score	828	827.6	812.8	747.8
	Result No.	7	7	т	4

877 UI-CF-EN: 056 RST2972 7 780 60158755: 536 603191255	EM682789 UL.E-EJI- BM719460 UI-E-EJI- B1495873 df121d04. B1091047 602855235 B1460319 602201967	AGEN AV647 ba59f RC3-	qe82d12. RC3-FN0 7j66c08 wg12e12.	400041	0 0121003 0 0566068 0 056603 0 0579928 0 0124-8W1 0 0124-8W1	BESSIESZ KOC-MIUUU AA79495 NW/8BO1.r BG189992 RST8946 A BU613909 UI-M-FRO- A1818729 WK91410.x AW052211 WY87406.x BQ033210 UI-1-CFO- A1126389 qC55e11.x AA204672 ZR7C06.r
BM98287 BG18405 BE79678 BI54853 BG21154	BM68278 BM71946 BI49587 BI09104 BI46031	BUS9107 AV647917 AW674008 BE83942 BIS4685	AI186701 BE83946 BF11468 AI800614		BU33208 AA746304 BU22529 BF73267 BF51315	AA797495 AA797495 BG189892 BU613909 AI818729 AW05211 BQ033210 AI126389 AA204672
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ALIGNMENTS

RESULT 1

	AK048800 2643 bp mRNA linear HTC 05-DEC-2002	Mus musculus 0 day neonate cerebellum cDNA, RIKEN full-length	enriched library, clone: C230071A14 product: inhibitor of growth	family, member 1-like, full insert sequence.	AK048800	AK048800.1 GI:26339579	HTC; CAP trapper.	Mus musculus (house mouse)	Mus musculus	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		Carninci, P. and Hayashizaki, Y.	High-efficiency full-length cDNA cloning	Meth. Enzymol. 303, 19-44 (1999)	99279253	10349636	6	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,	<pre>Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.</pre>	Normalization and subtraction of cap-trapper-selected cDNAs to	prepare full-length cDNA libraries for rapid discovery of new genes	Genome Res. 10 (10), 1617-1630 (2000)	20499374	11042159
AK048800	LOCUS	DEFINITION			ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM			REFERENCE	AUTHORS	TITLE	JOURNAL	MEDLINE	PUBMED	REFERENCE	AUTHORS		TITLE		JOURNAL	MEDLINE	PUBMED

REFERENCE AUTHORS

MEDLINE PUBMED REFERENCE AUTHORS

JOURNAL

TITLE

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/codon_start=1
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/db_xref="G1:66339580"
/trānslation="MLGQQQQQLYSSAALLTGERSRLLSCYVQDYLECVESLPHDMQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RNVSVLRELDNKYQETIJÆIDDVYSKYKKEDDSNQKKRLQQHLQRALINSQELGDEKI
QTUTQMLETUSNRARQMETHSQCRQDPAESRRASNSKSKNDSSQERRSREPRRQRYSE
SPILCHMTNOI DDCDDOPPERGXAKKKKRSKAKQEREASPVEFAIDPNETYCLC
NQVSYGANIGCDNEQCPIEWPHFSCVSLTYKFKGKWYCPKCRGDNEKTMDKSTEKTKK
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                                                                                                                                                                                                                                                                                                                                          /note="unnamed protein product; inhibitor of growth family, member 1-like (MGD|MGI:1916510, GB|NM_023503, evidence: BLASTN, 98%, match=971)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 2643;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 828; DB 11; Length 2
Pred. No. 1.2e-94;
0; Mismatches 118; Indels
                                                                                                                                                            /db xref="FANTOM DB:C230071A14"
/db_xref="taxon:10090"
/clone="C230071A14"
                                                                                                                                                                                                                                       /tissue type="cerebellum"
/clone Tib="RIKEN full-length
/dev_stage="0 day neonate"
476. 1321
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                                                                                        organism="Mus musculus"
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                                                                                                                     /mol_type="mRNA"
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88.3%;
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Best Local Similarity 88.3
Matches 933; Conservative
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Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Suni,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,B., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y. RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer

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Arakawa,T., Hara,A., Fukunishi,Y., Komo,H., Adachi,J., Fukuda,S.,
Aizawa,M., Isawa,M., Kiyosawa,H., Kondo,S., Yamanaka,I.,
Saito,T., Okazaki,Y., Gojobori,T., Bano,H., Kasukawa,T., Saito,R.,
Kadota,K., Matsuda,H., Ashburner,M., Batalov,S., Casavant,T.,
Fleischman,M., Gasterland,T., Gissi,C., King,B., Kochiwa,H.,
Kuchl,P., Lewis,S., Matsuo,Y., Nikaldo,I., Pesole,G.,
Ouackenbush,J., Schriml,L.M., Staubli,F., Suzuki,R., Tomita,M.,
Wagner,L., Washio,T., Sakai,K., Okido,T., Furuno,M., Aono,H.,
Baldarelli,R., Barsh,G., Bake,J., Boffelli,D., Bolunga,N.,
Fletcher,C., Fulta,M., Garibold,M., Gustincich,S., Hill,D.,
Hofmann,M., Hume,D.A., Kamiya,M., Lee,N.H., Lyons,P.,
Ring,B., Ringwald,M., Rodriguez,I., Sakamcto,N., Sasaki,H.,
Sato,K., Schonbach,C., Seya,T., Shibata,Y., Storch,K.F., Suzuki,H.,
Toyo-oka,K., Wang,K.H., Weitz,C., Whittaker,C., Wilming,L.,
Wynshaw-Boris,A., Yoshida,K., Hasegawa,Y., Kawaji,H., Kohtsuki,S.
and Hayashizaki,Y.
Functional annotation of a full-length mouse cDNA collection
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Please visit our web site for further details.
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URL:http://fantom.gsc.riken.go.jp/
Location/Qualifiers
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Group Phase I E II Team.

Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

I Nature 420, 563-573 (2002)

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E Adachl, J., Aizawa, K., Akimura, T., Hara, A., Hashizume, W., Hayashida, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramcto, K., Hiraoka, T., Hirozane, T., Katoh, H., Kawai, J., Kadua, N., Kadua, T., Kouda, M., Katoh, H., Kawai, J., Kondo, S., Konno, H., Kowai, J., Kojima, Y., Kondo, S., Konno, H., Kowai, J., Kojima, Y., Kondo, S., Konno, H., Sausi, K., Sakai, C., Sakai, K., Sakazume, N., Sakazume, N., Sakazume, N., Sakai, C., Sakai, K., Sakazume, N., Sakazume, N., Sakazume, N., Sakai, C., Sakai, K., Sakazume, N., Sagabe, Y., Tanaka, T., Tanaka, T., Tanaka, T., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M., and Hayashizaki, Y., Dincet Subnissia, M., Tanakai, Y., Tanaka, T., Towaru, A., Toya, T., Yasunishi, A., Direct Subnissia, M., A., Toya, T., Yasunishi, A., Direct Subnissia, M., Muramatsu, M., Malanatsu, M., A., Toya, T., Yasunishi, A., Direct Subnissia, M., Muramatsu, M., Malanatsu, M., Sakai, C., Yasunishi, A., Direct Subnissia, M., Muramatsu, M., Malanatsu, M., 
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/clone_lib="RIKEN full-length enriched mouse cDNA library"
/dev_stage="adult"
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Nature 409 (6821), 685-690 (2001)
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URL:http://genome.gsc.riken.go.jp/
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|db_xref="taxon:10090"
|clone="C630016P10"
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/strain="C57BL/6J"
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.009 ACCGAAAGAAAAGAGTCCAAGTCCGCCAAGAAGAAGAAGCGCTCCAAGGCCAAGCAGGA 1068
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                            Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new Genome Res. 10 (10), 1617-1630 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                     GTGCAGGGGAGATAATGAGAAAACAATGGACAAAAGTACTGAAAAAGACAAAAAAGGATAG
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2812 bp mRNA linear HTC 05-DEC-Mus musculus adult male hippocampus cDNA, RIKEN full-length enriched library, clone:C630016P10 product:inhibitor of growth family, member 1-like, full insert sequence.
                                                                                                                                                                                       718 CAACCAAGTGTCTTATGGGAGATGATAGGATGTGACAATGAACAGTGTCCAATTGAATG
                                                                                                                                                                                                                                                                                                                      GTTTCACTTTTCATGTGTTTCACTTACCTAAAACCAAAGGGGAAATGGTATTGCCCAAA
                                                               658 AAGGGAAGCTTCACCTGTTGAGTTTGCAATAGATCCTAATGAACCTACATACTGCTTATG
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y., Arakawa, T., Hara, A., Fukunishi, Y., Konno, H., Adachi, J., Fukuda, S., Arakawa, T., Hara, A., Fukunishi, Y., Kayosawa, H., Kondo, S., Yamanaka, I., Saito, T., Casati, Y., Gojobori, T., Bono, H., Kasukawa, T., Saito, R., Kadota, K., Matsuda, H., Ashburner, M., Batalov, S., Casavant, T., Fleischmann, W., Gasterland, T., Gissi, C., King, B., Kochiwa, H., Kuehl, P., Lewis, S., Matsuo, Y., Nikaido, I., Ruski, B., Kochiwa, H., Wagner, L., Washio, T., Sakai, K., Okido, T., Furuno, M., Aono, H., Baldarelli, R., Barsh, G., Blake, J., Boffelli, D., Bojunga, N., Carninci, P., de Bonaldo, M., Brownstein, M.J., Bult, C., Fujita, M., Gariboldi, M., Gustincich, S., Hill, D., Hofmann, M., Hume, D.A., Kamiya, M., Lee, N. H., Lyons, P., Marchionni, L., Mashima, J., Mazzarelli, J., Monbaerts, P., Nordone, P., Ring, B., Ringwald, M., Rodriguez, I., Sakamoto, N., Sasaki, H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus 10, 11 days embryo whole body cDNA, RIKEN full-length enriched library, clone:2810011M06 product:inhibitor of growth family, member 1-like, full insert sequence.

AK012716. I GI:12849649
HTC; CAP trapper.
Mus musculus (house mouse)
                                                                                                             1312 AAGAGCGAGGTAGTGAAGGCCATC--GGTTTTTAAAGGGTTCTTTGTTTTATAGAATTG 1369
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     GTTTGCTTTCAGAAATGTTTTAGGGTAAATGCATAAGACTATGCAATAATTTTAATCA
                                                                                                                                                                                                                           AAGATCGAGGTAGTAAAGGCCATCCACATTTTAAAGGGTTATTTGTCTTTTATATACTTC
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High-efficiency full-length cDNA cloning
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/translation="MiGQQQQQLYSSAALLTGERSRLLSCYVQDYLECVESLPHDMQ
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QTYQMLELLDNKYQETLKEIDDYPAESERASNGSWRDSSQPERSSRRPRQRTSE
SRDLCHMTNGIDDCDQPPKERSKGAKKKKRSKAKQBERASPVERAIDPNETYCLC
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                                                                                                                                                               The FANTOM Consortium and the RIKEN Genome Exploration Research Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

Nature 420, 563-573 (2002)

E 6 (bases 1 to 1464)

Rackawa,T., Bono,H., Carninci,P., Pukuda,S., Fukunishi,Y., Rono,H., Arakawa,T., Hori,F., Imotani,R., Ishi,Y., Itoh,M., Izawa,M., Hiraoka,T., Mori,F., Imotani,R., Ishi,Y., Itoh,M., Izawa,M., Kosukawa,T., Kato,H., Kawai,J., Kojima,Y., Konno,H., Kouda,M., Kosukawa,T., Mori,F., Imotani,R., Miyazaki,A., Nishi,K., Numazaki,R., Ohno,M., Okazaki,Y., Okido,T., Owa,C., Saito,H., Saito,R., Sakai,C., Sakai,K., Sano,H., Sastai,R., Sano,H., Sastai,R., Shibata,Y., Shibata,Y., Shibata,Y., Shibata,Y., Shibata,Y., Shibata,Y., Tagawa,A., Takahashi,F., Tanaka,T., Tejima,Y., Turimants,T., Waramata,T., Yasunishi,R., Yoshida,K., Yoshino,M., Muramatsu,W. and Hayashizaki,Y. Yoshida,K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Genomic Science Renter and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. First strand cDNA was primed with a primer [5, GAGAGAGAAGGATCCAAGAGCTTTTTTTTTTTTTTTTTVN 3], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. CDNA went through one round of normalization to Rot = 7.5 and subtraction to Rot = 37.5. Second strand cDNA was prepared with the primer adapter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIREN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Subhiro-cho, Tsurumi-ku, Yokohama, Kanagawa 210-0045, Japan (E-mail:Genome-res@gsc.riken.go.jp, NBL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,
Sato, K., Schonbach, C., Seya, T., Shibata, Y., Storch, K.F., Suzuki, H., Tryo-oka, K., Wang, K.H., Weitz, C., Whittaker, C., Wilming, L., Wynshaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawaji, H., Kohtsuki, S. and Hayashizaki, Y.
Functional annotation of a full-length mouse cDNA collection
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                                                               GCCTCAGATAAAGCAAAGATGGATTCCAGCCAACCAGAAAGATCTTCAAGAAGAACCCCGC
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                                       TGCGTGGAGTCGCTGCCCCACGACATGCAGAGGAACGTGTTGTGTTGTGCTGGAGAGGTGGAC
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McCray Lab
University of Iowa
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//organism="Homo sapiens"
//db Arsfe="texaon:9606"
/clone="InkagE:5810745"
/tissue_type="mixed (pool of 40 RNAs)"
/lab host="Bull08 (T1-phage-resistant)"
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/notary - 2.5%, liver - 5.7%, lung - 10.8%, NK-cell - 5.2%
/notary - 2.5%, prostate - 4.3%, salivary
/notary - 2.5%, prostate - 4.3%, salivary
/notary - 2.5%, pnnFnNF, Site_1: Sfil (ggccattatggcc);
/notary - 2.5%, pnnFnNF, Site_1: Sfil (ggccattatggcc);
/notary - 2.5%, pnnPnNF, Site_1: Sfil
                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

E 1 (bases 1 to 912)

S NIH-MGC http://mgc.nci.nih.gov/.

L Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: NCI
CDNA Library Preparation: Michael Brownstein Laboratory
CDNA Library Preparation: Michael Brownstein (LINL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
High quality sequence stops: 587.
                                                                                                                                                                         AGENCOURT 6738254 NIH_MGC_127 Homo sapiens cDNA clone IMAGE:5810745 BQ277444
  1366 TGCTTTACTTTCAGAAAATGTTTTAGGGTAACTGCATAAGACTATGCAATAATTTTTAAT 1425
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                                            1016 CATTAGTATTAATGGTGTATTAAAAGTTGTTGTACTTTG 1054
                                                                      1426 CATTAGTATTGATGGTGTATTAAAAGTTGTACTTTG 1464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 747.8; DB 13;
Pred. No. 2.2e-84;
0; Mismatches 22;
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Homo sapiens
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Best Local Similarity 96.9'
Marches 794; Conservative
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BQ277444
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ઠ g ઠે 256 877

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/mol_type="mRNA"

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/do_tref="Homo sapiens"

/do_tref="Homo sapiens"

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/clone_lib="Athersys RAGE Library"

/note="See" (Creation of Genome-wide Protein Expression

/inbraries using Random Activation of Gene Expression,

Nature Biotechnology, in press. Note that even though the

cell type indicated is HT1080, since a random activation

method was used, these sequence tags are not necessarily

expressed in HT1080 under normal circumstances."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BG184056 798 bp mRNA linear EST 21-APR-2001
RST2972 Athersys RAGE Library Homo sapiens CDNA, mRNA sequence.
BG184056
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Harrington, J.J., Sherf, B., Rundlett, S., Jackson, P.D., Perry, R., Cain, S., Leventhal, C., Thornton, M., Ramachandran, R., Whittington, J., Lerner, L., Costanzo, D., McElligott, K., Boozer, S., Mays, R., Smith, J., Veloso, N., Klika, A., Hess, J., Cothren, K., Lo, K., Offenbacher, J., Danzig, J. and Ducar, M.

Creation of genee-wide protein expression libraries using random activation of gene expression

Nat. Biotechnol. 19 (5), 440-445 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             998 TATGCAATAATTTTTAATCATTAGTATTAATGGTGTATTAAAAGTTGTTGTACTTTGAAA 1057
                                                                                                                                                                                                                                                                                                                                                        195 GAAAAGACAAAAAAGGATAGAAGATCGAGGTAGTAAAAGGCCATCCACATTTTAAAGGGTT 136
                                                                                                                                                                                                                                                         255 GGGAAATGGTATTGCCCAAAGTGCAGGGGAGATAATGAGAAAACAATGGACAAAAGTACT 196
                                                                                                                                                                                                                                                                                                                                                                                                           938 ATTTGTCTTTTATATAATTCGTTTGCTTTCAGAAAATGTTTTAGGGTAAATGCATAAGAC 997
                                                                                                                                                                                                                                                                                                                                                                                                                                                         135 ATTTGTCTTTTATATATTCGTTTGCTTTCAGAAAATGTTTTAGGGTAAATGCATAAGAC 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    75 TATGCAATAATTTTTAATCATTAGTATTAATGGTGTATTAAAAGTTGTTGTACTTTGAAA 16
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                         315 GAACAGTGTCCAATTGAATGGTTTCACTTTTCATGTGTTTTCACTTACCTATAAACCAAAG
                                                                                                                                                                                                          GAACCTACATACTGCTTATGCAACCAAGTGTCTTATGGGGAGATGATAGGATGTGACAAT
                                                                                                         GAACAGTGTCCAATTGAATGGTTTCACTTTTCATGTGTTTCACTTACCTATAAACCAAAG
                                                                                                                                                                                                                                                                                                            GAAAAGACAAAAAAGGATAGAAGATCGAGGTAGTAAAAGGCCATCCACATTTTAAAGGGTT
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Tel: 216 431 9900
Fax: 216 361 9596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          High quality sequence stop: !
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: scain@athersys.com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BG184056.1 GI:13705743
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/dev_stage="Adult"
/lab_host="DH108 (Life Technologies) (T1 phage resistant)"
/lab_host="DH108 (Life Technologies) (T1 phage resistant)"
/clone lih="UL-CF-EN1"
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Ul-CF-EN1 is a normalized CDNA library containing the following tissue(s): Primary Lung Cystic Fibrosis
Epithelial Cells. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:991-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded CDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligomucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is
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2024 University of Iowa Med Labs, Iowa City, IA 52242, USA Tel: 319 356 4866
Fax: 319 316 4866
Fax: 319 316 7171.
Email: paul-mccray@uiowa.edu
Tissue Procurement: Dr. M. J. Welsh, University of Iowa CDNA Library preparation: Dr. M. Bento Soares, University of Iowa CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa DNA Sequencing by: Dr. M. Bento Soares, University of Iowa Clone Distribution: Researchers may obtain clones from Research Genetics (www.resgen.com) or from Open Biosystems
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TAG_TISSUE=Human Lung Epithelial Cell Lines untreated LPS
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                                                                                                                                                                                                                                                                                                                                                        1. .735
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Cells"
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TAG_LIB=UI-CF-EN1
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68.1%; Score 735; DB 12;
Best Local Similarity 100.0%; Pred. No. 9.7e-83;
Matches 735; Conservative 0; Mismatches 0;
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_161 c 114 g
                                                                                                                                                                                                                                                      (www.openbiosystems.com).
Seg primer: M13 FORWARD
POLYA=Yes.
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/cione='rivade:3941035"
/tissue transe:3941031
/lab host='mHADB (phage-resistant)"
/clone lib="NHA MGC 7"
/cloned into EcoRI/XhoI sites using the following 5'
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Supersoript II RT (Life Technologies)."
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                                                                                                                Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLCM794 row: a column: 16
High quality sequence stop: 769.
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                                    NIH-WGC http://wgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (WGC)
Unpublished
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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Pred. No. 9.1e-80;
0; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                  organism="Homo sapiens"
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/db_xref="taxon:9606"
/clone="IMAGE:3941655"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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                                                                Gaps
                                                            2,
                        DB 10; Length 798;
                                                            Indels
                      Score 727.6; DB 10;
Pred. No. 7.7e-82;
0; Mismatches 4;
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8 8 8 8 8 8 8 8 8	6 8 6 8 6 8 6 8 6 8 6	DD RESULT 9 BG211544 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS TITLE JOURNAL
	RESULT 8 B1548536 B154866 B1548536 B154866 B1548536 B154866 B1548536 B154866 B15486 B1548	/ Organism="Homo sapiens" / mol_type="mRNA" / db_txref="taxon:9606" / clone="INAGE:5262540" / tissue_type="hippocampus" / lab_host="NHH_MGC_95" / clone=lib="NHH_MGC_95" / clone=lib="NHH_MGC_95"

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/dev stage="fetal and adult"
//dev stage="fetal and adult"
//lab_host="DH10B (Life Technologies) (T1 phage resistant)"
//clone_lib="UI-E-EJ1"
//note="Organ: eye, Vector: pT7T3-Pac (Pharmacia) with a
//organ: eye, Lennon and Soares, Genome Research,
//organ: eye subtracted = DNA library constructed
//organ: eye primer containing a Not I site. Double
//organic off primer containing a Not I site. Double
//organic off primer containing a Not I site. Double
//organic off primer containing a Not I site.
//organic off primer contained but a no pT7T3-Pac
//organic off primer containing a library tag sequence that is
//ocated between the Not I site and the (dT)18 tail. The
//organic organic 
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Tissue Procurement: Dr. Gregg Hageman
CDNA Library preparation: Dr. M. Bento Soares, Univeristy of Iowa
CDNA Library Arrayd by: Dr. M. Bento Soares, Univeristy of Iowa
DNA Sequencing by: Dr. M. Bento Soares, Univeristy of Iowa
Clone Distribution: Researchers may obtain clones from Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. [1 (bases 1 to 675) Bonaldo, M.F., Lennon, G. and Soares, M.B. Normalization and subtraction: two approaches to facilitate gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
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/db_xref="taxn=1506"
/clone="Ul-ExD1-3966"
/tissue_type="fetal eyes, lens, eye anterior segment,
optio_nerve, retina, Retina Foveal and Macular, RPE and
                       956 TCGTTTGCTTTCAGAAAATGTTTTAGGGTAAATGCATAAGACTATGCAATAATTTTTAAT
                                                                                                                896 AGAAGATCGAGGTAGTAAAGGCCATCCACATTTTAAAGGGTTATTTGTCTTTTATATAT
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UI-E-EJ1-ajf-g-22-0-UI.sl UI-E-EJ1 Homo sapiens cDNA clone
BM682789
                                                                                                                                                                                   771 CATTAGTATTAATGG-GGAATAAAAGTTGTTGACTTTGAAAAAAAA 818
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            University of Iowa 375 MEBRF, Iowa City, IA 52242, USA 375 Newton Road , 4156 MEBRF, Iowa City, IA 52242, USA Tel: 319 335 9565 Pax: 319 335 9565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Soares, MB
Coordinated Laboratory for Computational Genomics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genome Res. 6 (9), 791-806 (1996)
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Seg primer: M13 Forward
POLYA=Yes.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   63.0%; Score 680.8; DB 10; Length 919; 95.1%; Pred. No. 4.9e-76; ive 0; Mismatches 30; Indels 11;
                                                                     Athersys, Inc.
3201 carnegie Ave, Cleveland, OH 44115, USA
TTE1: 216 431 9900
Fax: 216 361 9596
                                                                                                                                                                                 High quality sequence stop: 439.
Location/Qualifiers
                                                                                                                                                                  scain@athersys.com
                     11329013
Contact: Scott J. Cain
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Matches 788;
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Choronomic Liberula and adult"

/ Lab_host="DH10B (Life Technologies) (T1 phage resistant)"

/ Clone libe-"Ull-E-EJ1"

/ Lote="Organ: eye; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site_1: EcoR I; Site_2: Not I; Ul-E-EJ1 is a subtracted cDNA library constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dr primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tags for this library are: fetal eyes, AGAATCAAGA; lens CGATTAGCGA; eye anterior segment, AATGCCGAT; optic nerve, CCATTAGCTG; retina, CGGGG, Retina Foveal and Macular, GTCC; RPE and Choroid, ACCTA. This library was created for the program, Gene Discovery in the Visual System, supported by National Eye Institute (NEI)."
                                                                                                                                                          377 GTTACACAAATGCTCGAATTGGTGGAAAATCGGGCAAGACAAATGGAGTTACACTCACAG 436
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                      1 (bases 1 to 664)
Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone="UI-E-EJI-ajf-g-22-0-UI"
/tissue type="fetal eyes, lens, eye anterior segment,
optic nerve, retina, Retina Foveal and Macular, RPE and
Choroid"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GTTACACAAATGCTCGAATTGGTGGAAAATCGGGCAAGACAAATGGAGTTACACTCACAG
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Pred. No. 9.8e-74;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                    Genome Res. 6 (9), 791-806 (1996) 97044477
                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
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Best Local Similarity 99.8%;
Matches 663; Conservative
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Macular, GTCC; RPE and Choroid, ACCTA. This library was created for the program, Gene Discovery in the Visual System, supported by National Eye Institute (NEI). TAG_LIB=UI_E-EJI
TAG_TISSUE=Foveal and Macular Retina TAG_ESC=GTCC"

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                             GTGGAAAATCGGGCAAGACAAATGGAGTTACACTCACCGTGTTTCCAAGATCCTGCTGAA
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                                                                                                                                                                                Score 671.8; DB 12; Length
Pred. No. 7.8e-75;
0; Mismatches 2; Indels
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ilarity 99.7%;
Conservative
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180

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BI091047 891 bp mRNA linear EST 20-JUN-2001
602855235F1 NIH_MGC_10 Homo sapiens CDNA clone IMAGE:4996593 5',
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                                                                                                                                                                                                                                                                                                                                                 653 AGTGTTTCCAAGATCCTGCTGAAAGGAACGAGCCTCAGATAAAGCAAAGATGGATTCCA
                                                                                                                                                                                                                                                                                                                                                                                                                               593 GCCAACCAGAAAGATCTTCAAGAACCCCCCCAGGCGGCGGCGGACCAGTGAAAGCCGTGATT
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                                                                                                                                                                                                                                                                                                                           AGTGTTTCCAAGATCCTGCTGAAAGTGAACGAGCCTCAGATAAAGCAAAGATGGATTCCA
                                                                                                                                                                                                                                                                                                                                                                                               GCCAACCAGAAGATCTTCAAGAAGACCCCGCAGGCAGCGGACCAGTGAAAGCCGTGATT
                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                      58.9%; Score 636.4; DB 12; Length 653; 99.8%; Pred. No. 2.1e-70; ive 0; Mismatches 1; Indels 0;
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Best Local Similarity 99.8
Matches 637; Conservative
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BI091047
BI091047.1 GI:1
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Brigham and Women's Hospital
75 Francis Street, Harvard Medical School, Boston, MA 02115, USA
761 Francis Street, Harvard Medical School, Boston, MA 02115, USA
77 To 17 28 6996
Fax: 617 738 6996
Email: occmorton@bics.bwh.harvard.edu
DNA sequencing and analyses were performed by National Institutes
of Health Intramural Sequencing Center (NISC; see
http://www.nisc.nih.gov).
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Plate: LLAM6327 row, G column: 7
Seq primer: T7 primer.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Districts, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.

1 (bases 1 to 653)

1 (bases 1 to 653)

2 (An Expertson, N. G., Khetarpal, U., Gutierrez-Espeleta, G.A., Bieber, F.R. and Morton, C.C.

1 solation of novel and known genes from a human fetal cochlear cDNA ilbrary using subtractive hybridization and differential screening Genomics 23, 42-50 (1994)
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df121d04.wl Morton Fetal Cochlea Homo sapiens cDNA clone
BI495873
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                                                                                     GAGTTTGCAATAGATCCTAATGAACCTACATACTGCTTATGCAACCAAGTGTCTTATGGG
                                                                                                                                     GAGATGATAGGATGTGACAATGAACAGTGCCAATTGAATGGTTTCACTTTTCATGTGTT
                                                                                                                                                       GAGATGATAGGATGTGACAATGAACAGTGTCCAATTGAATGGTTTCACTTTTCATGTGTT
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                                                                   GAGTTTGCAATAGATCCTAATGAACCTACATACTGCTTATGCAACCAAGTGTCTTATGGG
                                                                                                                                                                                                                                                                                                                                               CCATCCACATTTTAAAGGGTTATTTGTCTTTTATATAATTCGTTTGCTTTTCAGAAAATGT
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AAGTCAGCAAAGAAAAAAAAGCTCCAAGGCCAAGCAGGAAAGGGAAGCTTCACCTGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Morton, C. C. Departments of Pathology and Obstetrics, Gynecology and
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/mol__type="mRNA"
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Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
Toshiyuki and Piero Carninci (RIKEN)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.llh.gov
Plate: LLAM11675 row: f column: 18
High quality sequence stop: 700.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                    BI460319 708 bp mRNA linear EST 21-AUG-2001
603201967F1 NIH_MGC_97 Homo sapiens cDNA clone IMAGE:5267729 5',
                                                                                      GTACTGAAAAGACAAAAAAGGATAGAAGATCGAGGTAGTAAAAGGCCATCCACATTTTAAA 113
                                                                                                                            GGGTTATTTGTCTTTTATATAATTCGTTTGCTTTCAGAAAATGTTTTAGGGTAAATGCAT 992
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        232 CAAAGGGGAAATGGTATTGCCCAAAGTGCAGGGGAGATAATGAGAAAACAATGGACAAA 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       pBluescript KS+); Site 1: BamHI; Site 2: Sall-KhoI (gtcga ); Oligo-dT primed using primer 5'-TTTTTTTTTTTTTTTVN-3', saize-selected for average insert size 2.2 kb and normalized to ROT 5. This is a primary library enriched for full-length clones and constructed using the Cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NHM/NHGRI, National Institutes of Health). Note: this is a NIH MGC Library.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Buthoria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 708)
MIH-WGC http://mgc.noi.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
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/organism="Homo sapiens"

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:5267729"

/lab_host="MAGE:5267729"

/lobe_lost="MH MGC 97"

/note="Organ: testis; Vector: pBluescriptR (modified
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Pred. No. 9.2e-67;
0; Mismatches 6; Indels
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al Similarity 98.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      336 TAATTAATAGTCAAGAATTGGGAGATGAAAAATACAGA-TTGTTACACAAATGCTCGAA 394
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                                        Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                           Email: cgapber@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: Incyte Genomics, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/Link at:
http://image.llnl.gov
Plate: LiAMIN sequence stop: 722.
Location/Qualifiers
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NIH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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/organism="Homo sapiens"
                                                                                                                                                              Contact: Robert Strausberg, Ph.D.
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/lab_host="DH10B"
/clone_lib="NIH_MGC_10"
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                          CCGGCTGCTCACCTGCTACGTGCAGGACTACCTTGAGTGCGTGGGAGTCGCTGCCCCACGA
                                                                                                                                                                                                                                                                                                                                                               Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gerard Gradwohl (PNAS 97 P1607-1611, 2000)
cDNA Library Preparation: Catherine Lee, Endocrine Pancreas
Consortium
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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/db_xref="taxon:10090"
/clone="IMAGE:6430926"
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Location/Qualifiers 68..910 /*tag= a /product= "Tumour suppressor homologue protein, p33ING2" Tumour suppressor; p471NG3; cell proliferation; cellular aging; p331NG2; anchorage dependence; apoptosis; tumour; cancer; gene therapy; ds. Tumour suppressor homologue protein, p33ING2 DNA ALIGNMENTS (USSH) US DEPT HEALTH & HUMAN SERVICES. AAH03733 AAH28480 AAH28481 ABQ50058 ABQ50059 ABQ50060 ABQ50061 ABQ77429
AAT23370
AAK52101
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ABA08933
AAR90399
AAF90399 AAL37089 ABX60077 AAX28688 AAD12783 standard; DNA; 1080 BP 09-FEB-2001; 2001WO-US04425 09-FEB-2000; 2000US-0181292 23-OCT-2001 (first entry) Nagashima M; WO200159114-A2 Unidentified L6-AUG-2001 S S 236 236 197.2 183.8 183.8 183.8 183.8 183.4 183.4 183.4 183 182.4 182.2 142.6 125.8 125.8 124.6 124.6 101 101.4 98.8 143 AAD12783; Harris AAD12783 Human INGIL encodi Human INGIL encodi Human tumour suppr Human bone remodel Human secreted pro Human tumour suppr Murine P371NG1 cod Tumour suppressor January 12, 2004, 16:38:42; Search time 334 Seconds (without alignments) 8728.722 Million cell updates/sec Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. N Geneseq 19Jun03:*

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22: /SIDSI/gcgdata/geneseqf.embl/NA2001.DAT:* Description GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd. Total number of hits satisfying chosen parameters: 2552756 seqs, 1349719017 residues SUMMARIES Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries nucleic search, using sw model AAD12783 AAZ08596 AAZ08595 AAZ47473 AAS70424 AAC28459 AAZ47474 IDENTITY_NUC Gapop 10.0 , Gapext 1.0 В DB seq length: 0 DB seq length: 200000000 US-09-513-365A-2 1080 Length DB 840 11153 11154 346 325 2817 Query Match Title: Perfect score: 1046 838.4 825.2 825.2 332.2 325 253.6 Scoring table: Score

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                                                                                                                                                                                                                                                                    961 TGCTTTCAGAAAATGTTTTAGGGTAAATGCATAAGACTATGCAATAATTTTTAATCATTA
781 TCACTTTTCATGTGTTTCACTTACCTATAAACCAAAAGGGGAAATGGTATTGCCCAAAGTG
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                                                                                                                                             The present sequence is a DNA encoding tumour suppressor homologue protein, p31NG2 which is homologous to human tumour suppressor protein, p47NG3. The tumour suppressors of the invention are involved in the regulation of cell proliferation and in the control of cellular aging, anchorage dependence and apoptosis. The tumour suppressor protein, p47NG3, nucleic acids encoding it and antibodies against it are useful for diagnosis, prevention and treatment of tumours and cancers. The p471NG3 DNA is also used in gene therapy.
                                                                                                                                                                  protein,
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                                                                 protein p47ING3 for the diagnosis and treatment
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0; Mismatches 0;
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Best Local Similarity 100.0%;
Matches 1080; Conservative 0
                                                                                                                   Disclosure; Page 78; 80pp;
                                                                      suppressor
                     2001-488975/53
                    WPI; 2001-4889/3/
P-PSDB; AAE06675
                                                                   New tumor
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                                                                   96.9%; Score 1046; DB 20; Length 1078; llarity 99.5%; Pred. No. 4.9e-229; Conservative 0; Mismatches 5; Indels 0;
                                               Sequence 1078 BP; 356 A; 206 C; 280 G; 236 T; 0 other;
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925 ATCGAGGTAGTAAAGGCCATCCACATTTTAAAGGGTTATTTGACTATTATATAATCCGTT 984
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human tumour suppressor (TUSUP) nucleotide sequence.
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This sequence encodes the human tumour suppressor (TUSUP) protein. The TUSUP sequence was identified from a human lung cDNA library. The protein is 240 amino acids in length and has one potential cAMP and CGMP dependent protein kinase phosphorylation site, nine potential protein kinase phosphorylation sites, five potential casein kinase phosphorylation sites, and one potential tyrosine kinase phosphorylation sites, and one potential similarity to p33. TUSUP can be used to treat or prevent cancer, particularly of the reproductive or gastrointestinal tracts or of the immune system. Agonists of the TUSUP protein can be used to raise TUSUP specific antibodies and to screen for specific binding agents and potential therapeutic agents. The TUSUP nucleotide sequence can be used in gene therapy and as a source of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New human tumour suppressor protein for treating cancer, particularly reproductive and gastrointestinal tracts or immune system
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Pred. No. 1.3e-178;
0; Mismatches 18; Indels 0;
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                                         /note= "Tumour suppressor protein"
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TUSUE
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                                          Length 1154;
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                                                                      Indels
                 367 A; 216 C; 285 G; 265 T; 21 other;
                                         24;
                                         Score 825.2; DB 24;
Pred. No. 1.3e-178;
0; Mismatches 18;
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Conservative
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                                          TCCTAATGAACCTACATACTGCTTATGCAACCAAGTGTCTTATGGGGAGATGATAGGATG
                                                                                               TGACAATGAACAGTGTCCAATTGAATGGTTTCACTTTTCATGTGTTTCACTTACATAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to a combination comprising a number of substantially purified and isolated polynucleotides which are co-expressed with genes known to be involved in bone remodelling and osteoporosis. The invention is used to diagnose disorders associated with bone remodelling or osteoporosis, ABS70344-ABS70512 represent human bone remodelling genes of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A combination of polynucleotides which are co-expressed with genes known to be involved in bone remodeling and osteoporosis are useful an array for the diagnosis of bone remodeling and osteoporosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bone remodelling; osteoporosis; human; gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Column 239-242; 206pp; English.
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301 THNNTGTCACATGGCAAATGGGATTGAAGACTGTGATGATCAGCCA 346
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ່ວ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Patterson
                                                                                        AAZ47474 standard; cDNA; 325
                                                                                                                                                                                                                                                                                                                                                                                                    99WO-US11136.
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                                                                                                                                                               (first entry)
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Best Local Similarity 100.
Matches 325; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (INCY-) INCYTE PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fang YT, Corley NC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2000-062711/05
                                                                                                                                                                                                     Human tumour
                                                                                                                                                                                                                                                                                                                                                                                                    20-MAY-1999;
                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                             WO9961612-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                        28-MAY-1998;
                                                                                                                                                               14-MAR-2000
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                                                      RESULT 7
AAZ47474/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present sequence is one of a large number of 5' ESTs derived from mRNAs encoding secreted proteins. No ORF has yet been conclusively identified within the present sequence. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT primed cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer CDNA sequences have been obtained, the full 5' UTR is rarely included. S. ESTs are derived from mRNAs with intext 5' ends and the full 6' UTR is rarely included. Is EST sare derived from mRNAs and genomic DNAs. 5' ESTs are also need in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9
                                                                                        Human, 5' EST; expressed sequence tag; secreted protein; cDNA isolation; gene therapy; chromosome mapping; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AGCCAACCAGAAAGATCTTCAAGAAGACCCCGCAGGCAGCGGACCAGTGAAAGCCGTGAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                    New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedures
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 346 BP; 130 A; 63 C; 80 G; 70 T; 3 other;
                                                      Human secreted protein 5' EST, SEQ ID NO: 32534.
                                                                                                                                                                                                                                                                                                                                                                 Giordano J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; SEQ ID 32534; 71pp + CD-ROM; English.
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                                                                                                                                                                                                                                                                                                                                                                   Duclert A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       expression and secretion vectors.
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99.1%;
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                                                                                                                                                                                                                                                                                                                                                                 Dumas Milne Edwards J,
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                             (GEST ) GENSET
                                                                                                                                                                                                                                                                                         26-FEB-1999;
                                                                                                                                                Homo sapiens
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This sequence was used to determine the sequence of the human tumour suppressor protein (TUSUP) see AAY52199. The TUSUP protein is 240 amino acids in length and has one potential camp and GGMP dependent protein kinase bhosphorylation site, inne potential protein kinase c phosphorylation site, inne potential protein kinase phosphorylation site. TUSUP has sites, and one potential tyrosine kinase phosphorylation site. TUSUP has structural and chemical similarity to p33. TUSUP can be used to treat or prevent cancer, particularly of the reproductive or gastrointestinal used to raise TUSUP specific antibodies and to screen for specific binding agents and potential herapeutic agents. The TUSUP nucleotide sequence can be used in gene therapy and as a source of diagnostic probes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 910 GTAAAGGCCATCCACATTTTAAAGGGTTATTTGTCTTTTATAATTCGTTTGCTTTCAG 969
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New human tumour suppressor protein for treating cancer, particularly of reproductive and gastrointestinal tracts or immune system -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            145 GTAAAGGCCATCCACATTTTAAAGGGTTATTTGTCTTTTATATAATTCGTTTGTCTTTCAG
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                                                                                       Tumour suppressor protein; TUSUP; human; cancer; treat; prevent; reproductive tract; gastrointestinal tract; immune system; ss.
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suppressor (TUSUP) fragment nucleotide sequence.
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 AAAATGTTTTAGGGTAAATGCATAAGACTATGCAATAATTTTTAATCATTAGTATTAATG 1029
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mutations in or loss of the p53 gene occur in more than 50% of human tumours and tumour cell lines, but functional inactivation of the p53 pathway occurs in a much larger proportion of tumours. In many cases the mechanism of functional inactivation of the p53 gene remains unknown but p53 has been found to act in cooperation with ING1. Functional cooperation between ING1 and p53 suggested that ING1 encoded a tumour suppressor protein that functioned within the p53 pathway. This data suggested a possible role for ING1 in head and eck cancers and chromosomal location of the ING1 placed it within a region that is frequently rearranged in head and neck cancers. Large scale analysis of tumours involving ING1 has not revealed mutations in ING1 mor significant variations in its expression suggesting that ING1 was not a useful gene to study in cancer eriology. However, alternative initiation exons of the ing1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Detecting nucleic acid encoding exon 1b of ingl, useful for diagnosing and treating cancer, comprises contacting sample with isolated nucleic acid comprising sequence of exon 1b and detecting hybridized products
                   AAAATGTTTTAGGGTAAATGCATAAGACTATGCAATAATTTTTAATCGTTAGTATTAATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gene, each having their own promoter have been discovered.

Expression of one promoter (1a) produces a protein identical to INGI. Expression of a second promoter (1b) produces a protein having an identical C-terminal fragment to INGI but an additional 104

N-terminal amino acids. The newly discovered protein has been designated p371NGI wild type: p331NGI, p371NGI has the characteristics of an oncogene. When overexpressed in cells (even those expressing wild type p53) p371NGI is able to cause
                                                                                                                                                                                                                                                                      p53; tumour; cancer; detection; antibody; hybridisation; exon 1b; ING1; ing1; p331NG1; p371NG1; oncogene; gene therapy; diagnosis; proliferation disorder; transformation; transformed cell; mouse; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Grigorian IA;
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/product= P37ING1 polypeptide
                                                         1054
                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
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                                                        GTGTATTAAAAGTTGTTGTACTTTG
                                                                                 GTGTATTAAAAGTTGTTGTACTTTG
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                                                                                                                                                                                                                                         Murine P37ING1 coding sequence,
                                                                                                                                                        AAA53790 standard; cDNA; 2817
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1279 CCGAATAACAAGCGGTCCAGGAGGCAGCGAAACAATGAGAATCGAGAGAACGAGCGGTCGAAT 1338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1339 AATCACGACCATGATGACATCACCTCAGGAACGCCCAAGGAGAAGAAAGCAAAAACCTCA 1398
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     415
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TCGCTGCCCCACGACATGCAGAGGAACGTGTCTGTGCTGCGAGAGCTGGACAACAAATAT
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                           nucleic acid encoding exon 1b of ingl by hybridisation with an isolated nucleic acid having the sequence of exon 1b of ingl or its antisense sequence corn identify individuals expressing the oncogenic form of ingl. Novel peptide sequences taken from the 104 N-terminal peptide of p371NG1 can also be used to raise antibodies that can also be used in detection methods for the p371NG1 variant. The polypeptides may be useful in gene therapy for treatment of cell proliferation disorders, especially cancers and for diagnosing and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               33;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 2817;
   Thus detecting
                                                                                                                                                                                                                                                                                                                                                                                                                              Score 253.6; DB 21; Length
Pred. No. 5.8e-48;
0; Mismatches 289; Indels
                                                                                                                                                                                                                                                                                                                                                                Sequence 2817 BP; 670 A; 711 C; 846 G; 590 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CAAATGGAGTTACACTCACAGTGTTTCCAAGATCCTGCTGAAA-
proliferation or transformation of those cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GACAAAGCCCTGGAGAAGTCCAAGAAGAGAG 1670
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                                                                                                                                                                                                                                                                                                                                                                                                                                 23.5%;
60.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches 490; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
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p53; tumour; cancer; detection; antibody; hybridisation; exon 1b; ING1; ing1; p331NG1; p371NG1; oncogene; gene therapy; diagnosis; proliferation disorder; transformation; transformed cell; human; ds.
                                                                                                                                                                                                              Disclosure, Page 122-123; 134pp; English.
                                                                                                                                                         Gurova KV,
           BP
                                              Human P37ING1 coding sequence.
           standard; cDNA; 911
                                                                                                                     04-FEB-2000; 2000WO-US02959.
                                                                                                                                 99US-0118941
                                                                                                                                             (UNII ) UNIV ILLINOIS FOUND
                                   (first entry)
                                                                                                                                                         Zeremski M,
                                                                                                                                                                     WPI; 2000-491278/43.
                                                                                                                                                                           P-PSDB; AAY97244
                                                                                              WO200046370-A1
                                                                                                                                 04-FEB-1999;
                                                                                   Homo sapiens
                                   19-DEC-2000
                                                                                                          10-AUG-2000
                                                                                                                                                         Gudkov A,
                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
           AAA53792
                       AAA53792
RESULT 9
      AAA53792
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Mutations in or loss of the p53 gene occur in more than 50% of human tumours and tumour cell lines, but functional inactivation of the p53 pathway occurs in a much larger proportion of tumours. In many cases the mechanism of functional inactivation of tumours. In remains unknown but p53 has been found to act in cooperation with ING1. Functional cooperation between ING1 and p53 suggested that ING1 encoded a tumour suppressor protein that functioned within the p53 pathway. This data suggested a possible role for ING1 in head can encode a tumour suppressor protein that functioned within the p53 pathway. This data suggested a possible role for ING1 in head can encode and encoded and in sequently rearranged in head and neck within a region that is frequently rearranged in head and neck cancers. Large scale analysis of tumours involving ING1 has not expression suggesting that ING1 mor significant variations in its expression suggesting that ING3 was not a useful gene to study in cancer etiology. However, alternative initiation exons of the ing1 Detecting nucleic acid encoding exon 1b of ing1, useful for diagnosing and treating cancer, comprises contacting sample with isolated nucleic acid comprising sequence of exon 1b and detecting hybridized products gene, each having their own promoter have been discovered. Expression of one promoter (1a) produces a protein identical to 1NG1. Expression of a second promoter (1b) produces a protein having an identical C-terminal fragment to ING1 but an additional 104 N-terminal amino acids. The newly discovered protein has been designated p371NG1 (wild type: p331NG1). p371NG1 has the characteristics of an oncogene. When overexpressed in cells (even proliferation or transformation of those each cause proliferation or transformation of those cells. Thus detecting a nucleic acid encoding exon 1b of ing1 by hybridisation with an isolated nucleic acid having the sequence of exon 1b of ing1 or its antisense sequence can identify individuals expressing the oncogenic form of ingl. Novel peptide sequences taken from the 104 N-terminal peptide of p371NG1 can also be used to raise antibodies that can also be used in detection methods for the p371NG1 variant. The polypeptides may be useful in gene therapy for treatment of cell proliferation disorders, especially cancers and for diagnosing and Grigorian IA;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          325 CCAGAGAGCACTAATTAATAGTCAAGAATTGGGAGATGAAAAAATACAGATTGTTACACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               806 CAAGTGCCGGGGGGAACGAGAACACCATGGACAAAGCCCTGGAGAAATCCAAAAAAGA
                                                                                                                                                                                                                                                                GTCTGTGCTGCGAGAGCTGGACAACAATATCAAGAAACGTTAAAAGGAAATTGATGATGT
                                                                                                                                                                                                                                                                                                                         146 croccroarcegeadarceacegaaaraccaacaacaccegaagecracaccaage
                                                                                                                                                                                                                                                                                                                                                                                                                                                       385 AATGCTCGAATTGGTGGAAAATCGGGCAAGACAAATGGAGTTACACTCACAGTGTTTCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           715 ATGCAACCAAGTGTCTTATGGGGAGATGATAGGATGTGACAATGAACAGTGTCCAATTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              775 ATGGTTTCACTTTTCATGTGTTTCACTTACCTATAAACCAAAGGGGAAATGGTATTGCCC
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                                                                                                                                 CTACGTGCAGGACTACCTTGAGTGCGTGGAGTCGCTGCCCCCACGACATGCAGGAACGT
                                                                                                                                                                                             crareregaedeacraceacrecaredaerecerecerecerregaerregaearer
                                                                                                                                                                                                                                                                                                                                                                                        CTACGAAAAATATAAGAAAGAAGATGATTTAAACCAGAAGAAACGTCTACAGCAGCTTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  477 AAGCAAAGATGGATTCCAGCCAACCAGAAAGATCTTCAAGAAGACCCCGCAG--GCAGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              535 GACCAGTGAAAGCCGTGATTTATGTCACATGGCAAATGGGATTGAAGACTGTGATGATCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGAAAGGGAAGCTTCACCTGTTGAGTTTGCAATAGATCCTAATGAACCTACATACTGCTT
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                                                                     Gaps
                                                                     30;
      Score 237.4; DB 21; Length 911;
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                                                                     Indels
                                                                  0; Mismatches 291;
                                    1.9e-44;
                                    Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BP.
22.0%;
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                                                                  Matches 462; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 445 AGATC----
                                       Similarity
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         Query Match
                                       Best Local
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                                                                        852 CAAAGGGGAGGGGCAGGGAGGCTGACAAGCCCAACAGGGAAGCGCTCACGGC-GGCAGC 910
                                                                                                             GGACCAGTGAAAGCCGTGATTTATGTCACATGGCAAATGGGATTGAAGACTGTGATGATC 593
 792 GGCGCAGCAGCAGGCGGCGACACAGCGGGCAACAGCGGGCAAGGCTGGCGGCGCGACAGGCC 851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; gene; ss; monoclonal antibody; epitope; inhibitor of growth 1; ING1; tumour suppressor; cell cycle; breast tumour; lymphoid malignancy; cell growth; anti-ING1; CAb; isoform; diagnosis; tumour; antigen; p33ING1b.
                                                                                                                                               911 GCAACAACGAGAACCGTGAGAAACGCGTCCAGCAACCACGACCACGACGACGACGGCGCCTCGG
                                                                                                                                                                                                                                                            654 AGGAAAGGGAAGCTTCACCTGTTGAGTTTGCAATAGATCCTAATGAACCTACATACTGCT
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                                      594 AGCCACCTAAAGAAAAGAAATCCAAGTCAGCAAAGAAAAAGAAACGCTCCAAGGCCAAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human inhibitor of growth 1 (ING1) isoform, p33ING1b, cDNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence encodes a human cancer associated antigen. The sequence is a variant of the ING1 gene, which is a tumour suppressor gene candidate. The cancer associated antigen polynucleotides and polypeptides are useful for screening for the possible presence of a pathological condition in a subject such as cancer. The cancer associated antigen polypeptides are useful for producing vaccines.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CTACGTGCAGGACTACCTTGAGTGCGTGGAGTCGCTGCCCCCACGACGTGCAGGAACGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chen Y;
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                                                                                                                        Asn) "
Asp) "
Val) "
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Knuth A,
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(SLOK ) SLOAN KETTERING INST CANCER RES.
(CORR ) CORNELL RES FOUND INC.
                                  Location/Qualifiers
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24-OCT-2000; 2000US-0602362.
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Best Local Similarity 58.9°
Matches 462; Conservative
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P-PSDB; AAB84698.
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                                                                                                                                                                                                                                                                                                                                                                                         The invention discloses monoclonal antibodies which can be used, in combination, to specifically recognise epitopes of ING1 (inhibitor of growth 1) protein isoforms. ING1 is a tumour suppressor gene and its expression is regulated through the cell cycle, peaking in the S phase. Expression of ING1 is down regulated in breast tumours and lymphoid malignancies. Overexpression of a construct containing the ING1 gene is able to inhibit cell growth by reducing the fraction of cells which enter into the S phase. The monoclonal antibodies are useful for detecting an ING1 protein in a cell, which involves selecting a cell that ectopically or endogenously expresses ING1 protein. The anti-ING1 monoclonal antibody combination consists of two or more antibodies of CAbl-CAbl (not defined), preferably a mixture of CAbl-CAbd, which can detect at least two different isoforms of ING1. The antibodies are also useful for diagnosing a disease e.g. tumour or medical condition in an animal ansociated with abscrant levels of an ING1 protein. The sequence presented is the human inhibitor of growth I (ING1) isoform, 2007 and 20
                                                                                                                                  Novel monoclonal antibody which specifically recognizes epitope of ING1, inhibitor of growth 1 protein, and designated CAb1-10, useful for detecting two different isoforms of ING1 and diagnosing a medical
                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 10-12; 15pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protein used to raise antibodies.
                              2002-526652/56
                                                                 P-PSDB; AAU79587
                                                                                                                                                                                                                                                              condition
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Sequence 2897 BP; 733 A; 710 C; 819 G; 635 T; 0 other; Query Match 21.9*; Score 236; DB 24; Length 2897; Best Local Similarity 58.9*; Pred. No. 6.16-44; Matches 462; Conservative 0; Mismatches 290; Indels 32

1093 1153 1213 1332 974 CTCGCTGATGCGGGAGATCGACGCGAAATACCAAGAGATCCTGAAGGAGCTAGACGAGTG 1033 214 GGCGCAGCAGGAGCTGGGCGACACAGCGGCAACAGCGGCAAGGCTGGCGCGGACAGGCC 1273 GCAACAACGAGAACCGTGAGAACGCGTCCAGCAACCACGACCACGACGACGCGCCTCGG 1392 1393 GCACACCCAAGGAGAAGAAGGCCAAGACCTCCAAGAAGAAGAAGCGCTCCAAGGCCAAGG 1452 593 324 384 444 973 264 445 AGATC------CTGCTGAAAGTGAACGAGCCTCAG 473 713 914 CTATGTGGAGGACTACCTGGACTCCATCGAGTCCCTGCCTTTCGACTTGCAGAAAATGT GTCTGTGCTGCGAGAGCTGGACAACAAATATCAAGAAACGTTAAAGGAAATTGATGTGT CCAGAGAGCACTAATTAATAGTCAAGAATTGGGAGATGAAAAAAATACAGATTGTTACACA GATGGTGGAGCTGGAGAACCGCACGCGCAGGTGGACAGCCACGTGGAGCTGTTCGA 1274 CANAGGOGAGGOGGOGGOGGOGGOGGAGGOCCANCAGGAAGCGCTCACGGC-GGCAGC GGACCAGTGAAAGCCGTGATTTATGTCACATGGCAAATGGGATTGAAGACTGTGATGATC 654 AGGAAAGGGAAGCTTCACCTGTTGAGTTTGCAATAGATCCTAATGAACCTACATACTGCT CTACGTGCAGGACTACCTTGAGTGCGTGGAGTCGCTGCCCCACGACATGCAGGAACGT CTACGAAAAATATAAGAAAGAAGATGATTTAAACCAGAAGAAACGTCTACAGCAGCTTCT 385 AATGCTCGAATTGGTGGAAAATCGGGCAAGACAAATGGAGTTACACTCACAGTGTTTCCA AGCCACCTAAAGAAAAGAAATCCAAGTCAGCAAAGAAAAAGAAACGCTCCAAGGCCAAGC Gaps 32; Indels -0 Conservative 462; 1034 325 1154 1333 145 205 265 534 Best Loca Matches ò 셤 Š 셤 8 쉱 ð 셤 ò g à 셤 ò 임 ò a ò 셤 ઠે

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1453 CGGAGCGAGAGAGGCGTCCCCTGCCGACCATCGACCCAACGAACCCAACGTACTGTC 1512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Detecting nucleic acid encoding exon 1b of ingl, useful for diagnosing and treating cancer, comprises contacting sample with isolated nucleic acid comprising sequence of exon 1b and detecting hybridized products
                                                                                                                                                                                                                                                     1633 CCAAGTGCCGGGGGGAGAACGAGAAGACCATGGACAAAGCCCTGGAGAAATCCAAAAAAG
                                                                                                      1513 rerechacchestrerecraresesadarearesereceacaacaacaasacaares
                                                                                                                                             AATGGTTTCACTTTCACTTACCTAAAACCAAAGGGGAAATGGTATTGCC
                                                                                                                                                                                     1573 AGTGGTTCCACTTCTCGTGCGTGGGCCTCAATCATAAACCCCAAGGGCAAGTGGTACTGTC
                                                                                                                                                                                                                            834 CAAAGTGCAGGGGAGATAATGAGAAAACAATGGACAAAAGTACTGAAAAGACAAAAAAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            revealed mutations in ING1 nor significant variations in its expression suggesting that ING1 was not a useful gene to study in cancer etiology. However, alternative initiation exons of the ingl gene, each having their own promoter have been discovered. Expression of one promoter (la) produces a protein identical to ING1. Expression of a second promoter (lb) produces a protein having
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mutations in or loss of the p53 gene occur in more than 50% of the p53 pathway occurs in a much larger proportion of tumours. In many cases the mechanism of functional inactivation of the p53 gene remains unknown but p53 has been found to act in cooperation with ING1 Functional cooperation between ING1 and p53 suggested that ING1 encoded a tumour suppressor protein that functioned within the p53 pathway. This data suggested a possible role for ING1 in head and neck cancers and chromosomal location of the ING1 placed it within a region that is frequently rearranged in head and neck annexes. Large scale analysis of tumour involving ING1 has not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ING1; ing1; p331NG1; p371NG1; oncogene; gene therapy; diagnosis; proliferation disorder; transformation; transformed cell; mouse; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               p53; tumour; cancer; detection; antibody; hybridisation; exon 1b;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Grigorian IA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gurova KV,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Murine ingl common exon sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAA53789 standard; cDNA; 1835 BP
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                                                                                                                                                                                                                                                                                                                                                 1693 AGAG 1696
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BP.

AAH28479 standard; DNA; 1143

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an identical C-terminal fragment to ING1 but an additional 104
N-terminal amino acids The newly discovered protein has been
designated p3/ING1 (#11d type: p33ING1). p3/ING1 has the
characteristics of an oncogene. When overexpressed in cells (even
those expressing wild type p53) p3/ING1 is able to cause
those expressing wild type p53) p3/ING1 is able to cause
proliferation or transformation of those cells. Thus detecting a
nucleic acid encoding exon lb of ing1 by hybridisation with an
inclease sequence can identify individuals expressing the
oncogenic form of ing1. Novel peptide sequences taken from the 104
or its antisense sequence can identify individuals expressing the
oncogenic form of ing1. Novel peptide sequences taken from the 104
inclease of p3/ING1 can also be used to raise antibodies
that can also be used in detection methorapy for treatment of cell
the polypeptides may be useful in gene therapy for treatment of cell
proliferation disorders, especially cancers and for diagnosing and
                                                                                                                                                                                                                                                                                                                                                                                                                        306 AACGTCTACAGCAGCTTCTCCAGAGAGCACTAATTAATAGTCAAGAATTGGGAGATGAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAATACAGATTGTTACACAAATGCTCGAATTGGTGGAAAATCGGGCAAGACAAATGGAGT
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                                                                                                                                                                                                                                                                                                                                                DB 21; Length 1835;
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                                                                                                                                                                                                                                                                                                          Sequence 1835 BP; 541 A; 387 C; 468 G; 439 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TACACTCACAGTGTTTCCAAGATCCTGCTGAAA-----
                                                                                                                                                                                                                                                                                                                                              Score 197.2; DB 21;
Pred. No. 3.7e-35;
0; Mismatches 253;
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                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 58.5%;
Matches 399; Conservative
                                                                                                                                                                                                                                                                     studying cancers.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The sequence is the wildtype of the ING1 gene, which is a tumour suppressor gene candidate. The cancer associated antigen polymuclectides and polypeptides are useful for screening for the possible presence of a pathological condition in a subject such as cancer. The cancer associated antigen polypeptides are useful for producing vaccines.
                                                                                                               Cancer associated antigen; ING1; tumour suppressor; cancer; vaccine; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  194 AACAGATCCTGAAGGAGCTAGACGAGTGCTACGAGCGCTTCAGTCGCGGAGACGGGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chen Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Isolated cancer associated nucleic acid molecule identified by SERE) (serological identification of antigens by recombinant expression cloning) technique, useful in nucleic acid based therapies to treat
                                                                                                                                                                                                                                  Ala)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1143;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence encodes a human cancer associated antigen.
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                                                                                                                                                                                                                /transl_except= "(pos: 25..30, aa: Cys)"
/transl_except= "(pos: 124..126, aa: Pro,
/poroduct= "cancer assocciated antigen"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 183.8; DB 22; Length
Pred. No. 3.6e-32;
0; Mismatches 267; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gure
                                                                                   Nucleotide sequence of a human cancer associated antigen.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    old L,
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                                                                                                                                                                         cocation/Qualifiers
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57.0%;
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24-OCT-2000; 2000US-0602362
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Best Local Similarity 57.0
Matches 394; Conservative
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P-PSDB; AAB84697.
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                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (serological cloning) tech
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RESULT 13 AAH28479

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AAV62285 standard; cDNA; 1902
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                                     TCTTCAAGAA - - GACCCCGCAGGCAGCGGACCAGTGAAAGCCGTGATTTATGTCACATGG
                                                       494 CCAACAGCAAGCGCTCACGGCGGCAGCGCAACAACGAGAACCGTGAGAACGCGTCCAGCA
                                                                                            <u>AGAAAAAGAAACGCTCCAAGGCCAAGCAGGAAAGGGAAGCTTCACCTGTTGAGTTTGCAA</u>
                  434 ACAGCGGCAAGGTTGGCGCGGACAGGCCCAATGGCGATGCGGTAGCGCAGTCTGACAAGC
                                                                          CAAATGGGATTGAAGACTGTGATGATCAGCCACCTAAAGAAAAGAAATCCAAGTCAGCAA
                                                                                                                                                                                                                                                                                                                                                                                                                 Tumour suppressor gene, ING1, p33ING1, breast cancer, brain cancer, diagnosis, gene therapy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Isolated tumour suppressor gene, ING1 - useful to develop products for inhibiting or increasing cell proliferation, in particular for treatment or diagnosis of cancer
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P-PSDB; AAW19118.
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A partial cDNA clone (AAT69651), designated ING1, codes for a novel tumour suppressor protein p331NG1 (AAM19118) that is a potent inhibitor of cell growth. It was isolated by subtractive bybridisation between normal mammary and transformed epithelial cDNAs, isolation of an antisense ING1 cDNA insert that caused increased call profileration, and use of the insert that caused normal human fibroblast and HeLa cDNA libraries. A complete ING1 sequence (AAT69652) was obtd. by 5'RACE. ING1 is localised to the 11943-34 chromosome region, to which a number of human cancers have been mapped. ING1 nucleic acids can be used in the diagnosis of breast cancer; a decreased level of ING1 mRNA indicates cancerous cells. They can also be used in gene therapy methods to block the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 18; Length 1902;
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Pred. No. 4.3e-32;
0; Mismatches 267; Indels
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Best Local Similarity 57.0%;
Matches 394; Conservative
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ING1 gene; p331NG1; human; apoptosis; cell death; breast cancer;
brain tumour; gene therapy; tumour suppressor; ss.
                                            Location/Qualifiers
109..741
/*tag= a
                  Partial INGI partial cDNA sequence.
           18-JAN-1999 (first entry)
                                                                                                             P-PSDB; AAW79674
                                                                                                  Garkavtsev I,
                                                            WO9844102-A2
                                      Homo sapiens
                                                                           26-MAR-1998;
                                                                                   27-MAR-1997;
                                                                   08-OCT-1998
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Modulating eukaryotic apoptosis by increasing p331NG1 activity -using p331NG1 derivatives, to induce apoptosis in cancer cells, and in the investigation of apoptotic pathways
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                                                                                                                                                                                                                                                                                        Johnston RN, Riabowol K;
                                                                                                                                                                                   (UYTE-) UNIV TECHNOLOGIES INT INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 2; Fig 2; 66pp; English
98WO-CA00277
                                                                                                                                                                                                                                                                                   Helbing CC,
                                                                                                                                                                                                                                                                                                                                                                               WPI; 1998-542700/46.
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Following passage through a packaging line, normal mouse mammary applicabilatells were infected, and infected cells were infected into nude mice. Putative transforming fragments from tumours were isolated by PCR (see AAV62290-91) and subcloned into INCX. An ING1 fragment was obtained and used to screen normal human fibroblast and HeLa cell CDNA libraries. 2 Clones were sequence to obtain the partial ING1 sequence. The complete CDNA sequence (see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  involves administering an antisense oligonuclectide. Also claimed are a method for determining the apoptotic characteristics of a eukaryotic cell, an assay for determining the level of p33ING1 activity in a eukaryotic cell, and an isolated eukaryotic cell substantially free of p33ING1 biological activity. The invention discloses ING1 derivatives or variants that may be used to induce apoptosis in eukaryotic cancer cells.
                                                                                                                                                                                                                                                                                                                                                                                                         AAV62292) was obtained by RACE. A claimed method to potentiate apoptosis in a eukaryotic cell involves administering an active p33ING1 peptide or an oligonucleotide encoding such as a peptide. A claimed method for inhibiting apoptosis in a eukaryotic cell
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357 GAGATGAAAAATACAGATTGTTACACAAATGCTCGAATTGGTGGAAAATCGGGCCAAGAC 416
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                                                            <u> AGAAAAAGGATCCAAGGCCAAGCAGGAAAGGGAAGCTTCACCTGTTGAGTTTGCAA</u>
                                                                                                                                                                                                                  417 AAATGGAGTTACACTCACAGTGTTTCCAAGATC--------
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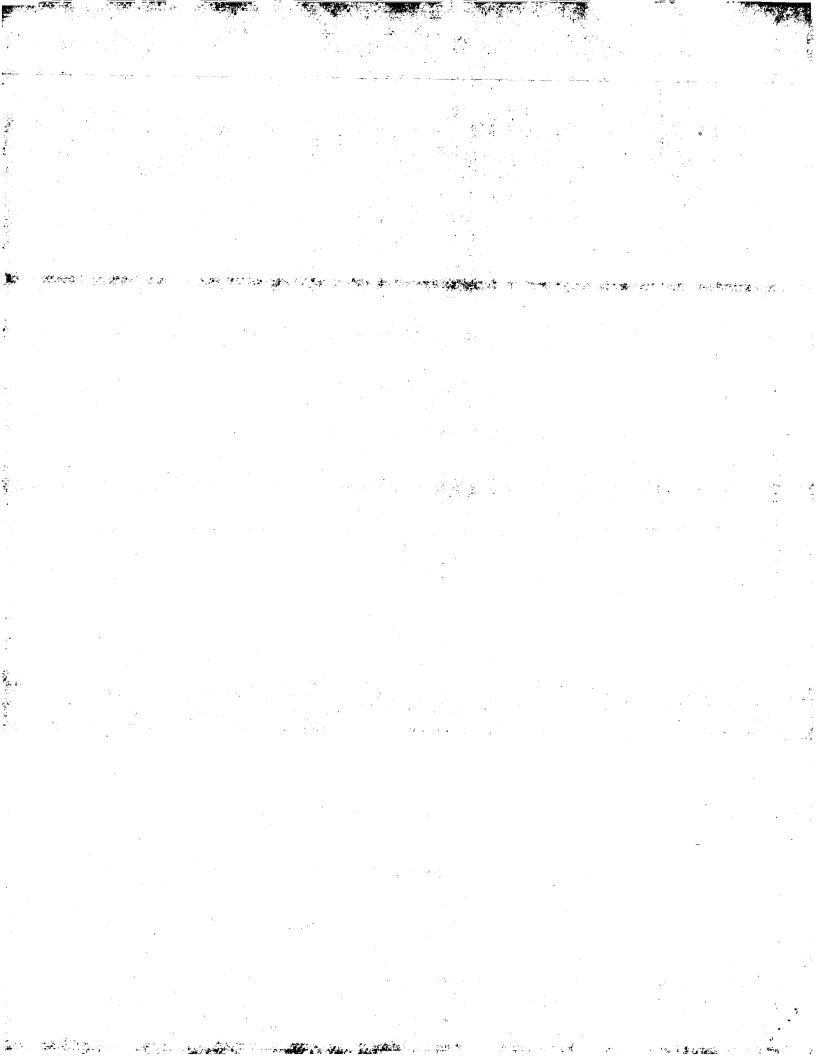
0; Mismatches 267; Indels 30; Gaps

DB 19; Length 1902;

17.0%; Score 183.8; DB 1 57.0%; Pred. No. 4.3e-32;

Matches 394; Conservative

Query Match Best Local Similarity



score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Run on:	January 12, 2004, 16:38:42; Search time 3978 S (without alignments) 11106.686 Million ce	ne 3978 Seconds gnments) llion cell updates/sec
Title: Perfect score: Sequence:	US-09-513-365A-2 1080 1 gcggccgcggtgcatgaaaaaa	ааааааааааааааааа 1080
Scoring table:	IDENTITY NUC Gapop 10.0 , Gapext 1.0	
Searched:	2888711 seqs, 20454813386 residues	
Total number of	f hits satisfying chosen parameters:	5777422
Minimum DB seg l Maximum DB seg l	length: 0 length: 2000000000	
Post-processing:	g: Minimum Match 0% Maximum Match 100% Listing first 45 summaries	
Database :	GenEmb1:*	
	2: gb_htg:* 3: gb_in:*	
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	30: em_htg_hum:*	
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AX211560 Sequence
AF053537 Homo sapi
BC030128 Homo sapi
AR012853 Homo sapi
AR012853 Homo sapi
AV016851 Homo sapi
AR213554 Sequence
AR220840 Sequence
AR220840 Sequence
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AR220840 Mus muscu
AC107214 Homo sapi
AF07284 Rattus no
AC102858 Rattus no
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AX367042 Sequence
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AC114475 Homo sapi
AX367043 Sequence
AR078440 Homo sapi
AR17755 Mus muscu
AC114756 Mus muscu
AC17756 Mus muscu ALIGNMENTS AF149820 BC016573 AF17757 HSING2S1 AF17184 AF149721 AF024401 AF024835 HSA310392 AF387042 AF18850 AC120896 AC120896 AC130896 AC130896 AC130896 AC130896 AC130896 AF078834 BC050003 AC132966 AC128348 AC094539 AC129658 AC107236 AC114762 AC098119 AY014017 BD052204 AR213555 AB012853 HSAJ6851 AR213554 AR220840 HSING2S2 AC107214 DB % Query Match Length D 96.9 77.8 843 76.4 115.7 115.7 183317 70.5 64.8 1262 63.6 245104 63.6 247796 63.6 247796 63.6 247796 63.6 247796 63.6 247796 63.6 63.7 64.8 63.6 64.8 63.6 64.8 64.8 63.6 64.8 64. 21.9 845 21.9 1533 22.9 2897 19.2 201302 19.2 222955 18.4 184918 18.4 1959 18.4 1959 18.3 1944 17.1 822331 199 199 198.8 197.8 192 Result No. OU

	linear PAT 06-SEP-2001							ebrata; Euteleostomi;	minidae; Homo.					
	1080 bp DNA 1	ent W00159114.		13814				Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	Primates; Catarrhini; Ho		jashima, M.	gene, p47ing3	A 7 16-AUG-2001;	
	AX211560	Sequence 7 from Patent WO0159114.	AX211560	AX211560.1 GI:15523814		Homo sapiens (human)	Homo sapiens	Eukaryota; Metazoa;	Mammalia; Eutheria;	1	Harris, C.C. and Nagashima, M.	Tumour suppressor g	Patent: WO 0159114-A 7 16-AUG-2001;	
AX211560	rocns	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM			REFERENCE	AUTHORS	TITLE	JOURNAL	

Pred. No. is the number of results predicted by chance to have a

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Nagashima, M., Shiseki, M., Miura, K., Hagiwara, K., Linke, S.P., Pedeux, R., Wang, X.W., Yokota, J., Riabowol, K. and Harris, C.C. DNA damage-inducible gene p33ING2 negatively regulates cell proliferation through acetylation of p53
Proc. Natl. Acad. Sci. U.S.A. 98 (17), 9671-9676 (2001)
                                                                                                                  TGCTTTCAGAAAATGTTTTAGGGTAAATGCATAAGACTATGCAATAATTTTTAATCATTA
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Submission
Submitted (12-MAR-1998) Laboratory of Human Carcinogenesis,
National Cancer Institute, 37 Convent Drive Bldg.37 Rm.2C01,
Bethesda, MD 20892, USA
Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 1.2e-221;
Matches 1080; Conservative 0; Mismatches 0;
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THE DEPARTMENT OF HEALTH AND HUMAN SERVICES
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Pred. No. 1.2e-221;
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                   Location/Qualifiers
1. 1080
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/codon_start=1
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QVSYGEMIGCDNEQCPIEWFHFSCVSLTYKPKGKWYCPKCRGDNEKTMDKSTEKTKKD
                                                                                                                                                                                                                                                                                                                                                                                                                                      Web site: http://www.nisc.nih.gov/
Contact: nisc_mgc@nhgri.nih.gov/
Akhter,N., AeTele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
Dietrich,N.L., Granite,S., Guan,X., Gupca,J., Haghighi,P.,
Hansen,N., Ho,S.-L., Karlins,E., Laric,P., Legaspi,R., Maduro,Q.L.,
Massiello,C., Maskeri,B., Mastrian,S.D.,McCloskey,J.C., McDowell,J.,
Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W., Tsurgeon,C.,
Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L., Young,A.,
Zhang,L.-H. and Green,B.D.
      PRI 20-MAY-2002
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This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 4504694.
Location/Qualifiers
                                                                                                                                        Euteleostomi;
                                                                                                                                                                                                  Direct Submission
Submitted (07-MAY-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                      member 1-like, clone
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                                                                                                                                                                                                                                                                                                   Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
CDNA Library Preparation: Wulin Laboratory
DNA Library Arrayed by: The I.M.G.E. Consortium (LLNL)
Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
                                                                                                                               Eukaryoča, Metazoa, Chordata, Craniata, Vertebrata, Butele
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 1141)
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/clone lib="NHH MGC 7"
      linear
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                  Homo sapiens, inhibitor of growth family, mer
MGC:10524 IMAGE:3941655, mRNA, complete cds.
                                                                                                                                                                                                                                                                                     NIH-MGC Project URL: http://mgc.nci.nih.gov
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Best Local Similarity 100.0%; Pred. No. 3.8e-220;
Matches 1073; Conservative 0; Mismatches 0;
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/db_xref="LocusID:3622"
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inhibitor of growt
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                                                                      BC030128.1 GI:20987212
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   GCGGCCGCCGCTGCATGTGCGGCTGCTGGATGCGGAGGCGGCGGCGACGCCGCGGAT
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                                                                                                  GGAGCGGAGCCGGCTGCTCCTGCTACGTGCAGGACTACCTTGAGTGCGTGGAGTCGCT
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December 96.9%; Score 1046; DB 9; Length 1078;	241 AACGITAAAGGAAATTGATGATGATGAAAATTAAAGAAGAAGAAG	625 TAAAGAAAAGAAATCCAAGTCAGCAAAAAAAAAAGAAAACGCCCAAGCACCAAGCACCAAGCACCAAGCAGC
Qy 781 TCACTTTCATGTGTTTCACTTACCTATAAACCAAAGGGGAAATGGTATTGCCCAAAGTG 840 Db 805 TCACTTTCATGTGTTTCACTTACCTATAAACCAAAGGGGAAATGGTATTGCCCAAAGTG 864 Qy 841 CAGGGGAGATAATGAGAAACAAAGTACTGAAAAGACAAAAAGGATAGAAG Bb 865 CAGGGGAGATAATGAGAAACAATGGACAAAAGTACTGAAAAAGACAAAAAAGATACTATAAAAAAGATACAAAAAAAA	RESULT 5 AB012853 LOCUS DEFINITION Home sapiens ING1L mRNA for ING1Lp, complete cds. VCCESSION VECKSION VECKSION VECKSION NULLP SOURCE Home sapiens GRANISM GRANISM HOME Sapiens GRANISM HOME Sapiens GRANISM HOME Sapiens JOURNAL JOURNAL JOURNAL GYLOGENET. Cell Genet. 83 (3-4), 232-235 (1998) HOME SAPIENCE AUTHORS AUTHOR	PEATURES COMMENT Sequence updated (17-Apr-1998). FEATURES SOURCE 1. 1078 1. 1078 1. 1078 Ab Xref="taxon:9606" Aproxosome="4" Amap="4435.1" Adv_stage="fetal" Alson="1.078" 1. 1078 CDS 92. 934 product="INGIL" Codon_start=1 product="INGQQQQLYSSAALLTGERSRLLTCYVQDYLECVESLPHDMQR NVSVLRELDNWYRARQMELHESCPTAREIDDYREKREDEES PLOWINGEREDNWYRENGORESES RDLCHMANGIEDCDDQPPREKKSRSARKKRSSARREPRGFISES RDLCHMANGIEDCDDQPPREKKSRSARKRESPVEFAIDPNEFTYCLCN RRSR RRSR

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                 ATACAGATTGTTACACAAATGCTCGAATTGGTGGAAAATCGGGCAAGACAAATGGAGTTA
                                                                                                                                 601 TCACCTGTTGAGTTTGCAATAGATCCTAATGAACCTACATACTGCTTATGCAACCAAGTG
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                                                       CACTCACAGIGITICCAAGAICCTGCTGAAAGIGAACGAGCCTCAGAIAAAGCAAAGAIG
                                                                                                             GATTCCAGCCAACCAGAAGATCTTCAAGAAGACCCCGCAGCGGACCAGTGAAAGC
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1 (Dases 1 to 840)
Nagata,M., Ozaki,K., Shimada,Y. and Horie,M.
Isolated DNA molecule encoding human TSC403
Patent: US 6403785-A 6 11-JUN-2002;
Location/Qualifiers
1. 840
/organism="unknown"

T 297 a 164 c 211 g 168 t
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Pred. No. 9.6e-170;
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NVSYLRELDNKYQETLKEIDDYYEKYKKEDDLMQKKRLQQLLQRALINSQELGDEKIQ
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RDLCHWANGTEDCDQQPREKKSKAKKKRSKAKQEREASVWEFAIDPNBFTYCLCN
QVSYGEMIGCDNEQCPIEWFHPSCVSLTYKPPKGKWYCPKCRGDNEKTMDKSTEKTKKD
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                                                                                                 PRI 06-JAN-2001
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Submitted (08-JUN-1998) Lopez-Otin C., Bioquimica y Biologia
Molecular, Universidad de Oviedo. Facultad de Medicina., C/ Julian
Claveria s/n., 33006, SPAIN
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Pred. No. 4.8e-170;
0; Mismatches 2;
                1045 GTATTAATGGTGTATTAAAAGTTGTACTTGT 1078
  GTATTAATGGTGTATTAAAAGTTGTTGTACTTTG 1054
                                                                                                                                                                                                                                       Cal,S., Freije,J.M. and Lopez-Otin,C.
ING2,a new possible gene supressor tumor
Unpublished
2 (bases 1 to 843)
                                                                                                   mRNA
                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
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/db_xref="taxon:9606"
/tissue_type="breast tumor"
1. .843
/gene="ing2"
                                                                                          NA Homo sapiens mRNA for p32 protein.
AJ006851
AJ006851; GI:12053587
ing2 gene; p32 protein.
Homo sapiens (human)
Thomosapiens
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/protein_id="CAC20567.1"
/db_xref="G1:12053588"
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/codon_start=1
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il Similarity 99.8%;
841; Conservative
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Mammalia; Eutheria;
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Qy 188 GACATGCAGAGGAACGTGTCTGTGCTGCAGAGCTGGACAAATATCAAGAAACGTTA 247 Db 121 GACATGCAGGAACGTGTCTGTGCTGCGAGAGCTGGACAAATATCAAGAAACGTTA 180 Qy 248 AAGGAAATTGATGATGTCTACGAAAATTAAAAAAGAAAAGAATTAAAACAGAAAAAA 307 Db 181 AAGGAAATTGATGATGTCTACGAAAAATATAAGAAGAAGAGATGAAAAA 240 Qy 308 CGTCTACAGCAGTTCTCCAGAAGAGCACTAATTAATAGTCAAGAATTGGGAGAAGAAAA 367 Db 241 CGTCTACAGCAGCTTCTCCAGAAGAGCACTAATTAATAGTCAAGAATTGGGAGATGAAAAA 300 Db 241 CGTCTACAGGAGTTCTCCCAGAGGACACTAATTAATAGTCAAGAATTGGGAGATGAAAAA 300	Oy 368 ATACAGATTGTTACACAAATTGCTCGAATTGGTGGAAAATCGGCAAGACAAATGGAGTTA 427 Db 301 ATACAGATTGTTACACAAATGCTCGAATTGGTGGAAAATCGGGCAAGACAATGGAGTTA 360 Qy 428 CACTCACAGTGTTTCCAAGATCCTGCTGAAAGTGAACGAGCTCAGATAAAGCAAAGATG 487 Ab 361	488 GATTCCAGCCAACCAGAAAGATCTTCAAGAAGACCCGCAGGCAG	AAGAAATCCAAGTCAGCAAAGAAAAAGGAAACGTTCCAAGGCCAAGCAGGAAAGGGAAGGT	Db 601 TCACCTGTTGCAATAGATCCTAATGAACCTACATACTTATGCAACCAAGTG 660 Qy 728 TCTTATGGGGAGATGATAGGATGTGAAAGAACAGTGTCCAATTGAATGGTTTCACTTT 787 Db 661 TCTTATGGGGAGATGATGAGATGTGACAATGAACAGTGTCCAATTGAATGGTTTCACTTT 720	OY 788 TCATGTGTTTCACTTACAAAACCAAAGGGAAATGGTATTGCCCAAGTGCAGGGA 847		SOURCE Unknown. ORGANISM Unknown. Unclassified. REFERENCE 1 (bases 1 to 1154) AUTHORS Jones, K.A., VOLKmuth, W. and Walker, M.G.	AL S urce UNT	Query Match 76.4%; Score 825.2; DB 6; Length 1154; Best Local Similarity 97.9%; Pred. No. 7e-167; Matches 836; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

us-09-513-365a-2.rge

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AC107214 15-OCT-2002
Homo sapiens BAC clone RP11-367N14 from 4, complete sequence.
AC107214
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University School of Medicine, 4444 Forest Park Parkway, St. Louis,
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                                                                                                                                                   GAATGGTTTCACTTTTCATGTGTTTCACTTACCTATAAACCAAAGGGGAAATGGTATTGC 832
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Catarrhini, Hominidae, Homo.
                                   GAATGGTTTCACTTTTCATTTCACTTTCACTTACCTATAAACCAAAGGGGAAATGGTATTGC
                                                                                                                                                                                                                        CCAAAGTGCAGGGGAGATAATGAGAAACAATGGACAAAAGTACTGAAAAAGACAAAAAG
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                                                                                  TTATGCAACCAAGTGTCTTATGGGGAGATGATAGGATGTGACAATGAACAGTGTCCAATT
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Submitted (16-JAN-2002) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St.
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Nguyen,C., Haglund,K. and Spalding,L.

The sequence of Homo sapiens BAC clone RP11-367N14

Upublished (2001)

3 (bases 1 to 183317)
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Genome Res. 8 (11), 1097-1108 (1998)
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Sulston, J.E. and Waterston, R.
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4 (bases 1 to 183317)
Waterston, R.H.
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6 (bases 1 to 183317)
Waterston, R.
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Homo sapiens
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QVSYGEMIGCDNGQCPIEWFHFSCVSLTYKPKGKWYCPKCRGDNEKTMDKSTEKTKKU
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.

1 (bases 1 to 974)
Nagashima, M., Hadiwara, K., Minter, A.R. and Harris, C.C.
Direct Submission
Submitted (101-MAY-1998) Laboratory of Human Carcinogenesis, National Cancer Institute, 37 Convent Dr. Bidg.37, Rm.2C26, Bethesda, MD 20892, USA
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Pred. No. 3.6e-165;
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                                                                      Submitted (15-OCT-2002) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA On Sep 20, 2002 this sequence version replaced gi:20128734.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see http://genme.wustl.edu/gsc
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA 7 (bases 1 to 183317)
                                                                                                                                                                                                                                                                                                     NOTICE: This sequence may not represent the entire insert of this form. I may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.
                                                                                                                                                                                                                                                                                                                                                                                                                     all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as Compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The RPCI-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Frengen, E. Tateno, M., Catanese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong and coworkers at http://www.chori.org
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This sequence is the entire insert of the clone. This clone is
overlapped by AC112698.
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                                                                                                                                                                                                                                                                                                                                                                                                 This sequence was finished as follows unless otherwise noted:
                                                                                                                                                   Center: Washington University Genome Sequencing Center
Center code: WUGSC
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                                                                                                                                                                                       Web site: http://genome.wustl.edu/gsc
Contact: sapiens@watson.wustl.edu
                                                                                                                                                                                                                              Center project name: H_NH0367N14
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                                                         Direct Submission
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Nagashima,M., Hagiwara,K., Hancock,A.R. and Harris,C.C.
Direct Submission
Submitted (16-7UL-1998) Laboratory of Human Carcinogenesis, Submitted (16-7UL-1998) Laboratory of Human Carcinogenesis, National Cancer Institute, National Institutes of Health, 37
Convent Dr., Bldg. 37, Rm. 2C01, Bethesda, MD 20892, USA
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Mus musculus p331NG2 (Ing2) mRNA, complete cds.
AF078834
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Pred. No. 3.5e-153;
0; Mismatches 111; Indels
                                                                                                                                                                                                                                                                                                                              /organism="Mus musculus"
/mol type="mRNA"
/db_rref="taxon:10090"
1. 1001
/gene="Ing2"
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                                                                                                                                         Mus musculus (house mouse)
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Best Local Similarity 88.1%;
Matches 887; Conservative
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/gene="Ing2'
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                                                                                                                                                                                                                      Score 817.2; DB 9;
Pred. No. 1.1e-164;
0; Mismatches 3;
                                                                                                                                                                   23<u>1</u>8<u>2</u>. .2<u>3</u>212
/rpt_family="(TAAA)n"
                                                                                              /2432. .25526
/rpt_family="MIR"
/3055. .23181
                                                                                                                               /rpt_family="Alu"
/s3182, 23181
/rpt_family="Alu"
21605. .21740
/rpt_family="Alu"
21746. .22060
                                                           /rpt_family="Alu"
22072. .22381
/rpt_family="Alu"
22432. .22526
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Best Local Similarity 99.6%;
Matches 819; Conservative
                repeat_region
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/translation="MLGQQQQQLYSSAALLTGERSRLLTCYVQDYLECVESLPHDMQ
RNVSYLRELDNKYOFTLKEIDDYZRKYKKEDDSNOKKRLQOHLQRALINSOELGDEKI
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SRDLCHWTNGIDDCDQPPKERRSKKKKKSKAKQERSPYERAIDPNEPTYCLC
NQVSYGEMIGCDDEQCPIEWPHSCVSLTYKPKGKWYCPKCRGDDEXTWDKSTEKTKK
Dietrich, N. L., Granite, S., Guan, X., Gupta, J., Haghighi, P., Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Laric, P., Legaspi, R., Maduro, Q.L., Masiello, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C., McClowell, J., Pearson, R., Stantripop, S., Thomas, P. J., Touchman, J.W., Tsurgeon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L., Young, A., Zhang, L.-H. and Green, E.D.
                                                                                                                              Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: http://image.llnl.gov Series: IRAK Plate: 108 Row. o Column: 20 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 12963706.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /codon_start=1
/product="Similar to inhibitor of growth family, member
1-like"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 700.2; DB 10;
Pred. No. 5.3e-140;
0; Mismatches 120;
                                                                                                                                                                                                                                                                                                                    /db_xref="taxon:10090"
/clone="IMAGE:6515125"
/tissue type="Mammary tumor. Mmold mouse. Taken by biopsy."
/clone lib="NCI CGAP_Mam2"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="Vector: pCMV-SPORT6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /protein_id="AAH50003.1"
/db_xref="GI:29436710"
                                                                                                                                                                                                                                                                 /organism="Mus musculus"
                                                                                                                                                                                                                              Location/Qualifiers
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                                                                                                                                                                                                                                                                                    /mol_type="mRNA"
/strain="FVB/N-3"
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Best Local Similarity 86.6%;
Matches 780; Conservative
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 1262)
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Contact: nisc_mgc@nhgri.nih.gov
Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
Blakesley,R.W., Bouffard,G.G., Breeh,K., Brinkley,C., Brooks,S.,
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Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                   GTCGAAGATGGATTCCAGTCAACGGAAAGATCTTCTAGAAGACCTCGAAGACAGAGGAC
                                                                                                                                                                           CAACCAAGTGTCTTATGGGGAGATGATAGGATGTGACAATGAACAGTGTCCAATTGAATG
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AAGGGAAGCTTCACCTGTTGAGTTTGCAATAGATCCTAATGAACCTACATACTGCTTATG
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
Gaithersburg, Maryland;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
Submitted (31-MAR-2003) National Institutes of
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Mus musculus, Similar to inhibitor
clone IMAGE:6515125, mRNA, partial
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Submitted (05-SEP-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

Sat Genome Sequencing Consortium.

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S. Rat Genome Sequencing Consortium.

AL Submitted (19-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

On Nov 19, 2002 this sequence version replaced gi:23264819.

The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas and whole genome shotgun sequencing reads assembled using Atlas and whole sequence contigs are contered, and separated in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads.
                 Dichibilities J. D. Doulsegor, D. Doulsegor, D. Doulsegor, D. Doulsegor, D. Doulsegor, D. Doulsegor, D. Martino, K., Martinok, C., Mandhadarino, Mandhadarinok, Martinok, Martinok, Mandhadarinok, Mandhadarinok, Mandhada, D. Machada, D. Mandhada, D. Montenayor, J. Moore, S., Milosavljevic, A., Miner, G., Minia, B., Montemayor, J., Moore, S., Morgan, M., Morris, K., Morris, S., Munidasa, M., Murphy, M., Nair, L., Nankeris, C., Neal, D., Newton, N., Nguyen, N., Norris, S., Nankeris, C., Deuton, G., Olarnpunsagon, A., Pal, S., Parks, K., Patscherak, S., Paul, H., Perez, L., Pefannkoch, C., Patkerrak, S., Paul, M., Perez, D., Primus, B., Pul, L.-L., Plopper, F., Poindexter, A., Popovic, D., Primus, B., Pul, L.-L., Patschin, B., Reeves, K., Regier, M., Reigh, R., Reilly, B., Reilly, M., Ren, Y., Reuter, M., Richards, S., Shen, H., Sanders, W., Saherer, S., Scott, G., Shatsman, S., Shen, H., Shetty, J., Shvartsbeyn, A., Sisson, I., Sitter, C.D., Smajs, D., Steimle, M., Strong, K., Sutton, A., Svatek, A., Tabor, P., Taylor, C., Taylor, T., Thomas, M., Thomas, D., Tingey, A., Trejos, Z., Usmani, K., Valas, R., Valas, M., Walker, B., Wang, J., Williama, G., Williama, D., Waldron, L., Walker, B., Wang, J., Williama, G., Williama, D., Waldron, L., Walker, B., Wang, J., William, G., William, G., William, G., William, C., Wi
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Center code: BCM
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Direct Submission
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Rattus norvegicus clone CH230-210B24, WORKING DRAFT SEQUENCE, 2
Unordered pieces.
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae,
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HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
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* NOTE: Estimated insert size may differ from sequence length

* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank draft_data.html).

* NOTE: This is a 'working draft' sequence. It currently

* consists of 2 contigs. The true order of the pieces

* is not known and their order in this sequence record is Web site: http://www.hgsc.bcm.tmc.edu/

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Eukaryota; Metazoa;
Mammalia; Eutheria;
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complement(218103, .218757)
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RATCHES.

18 Marzy D. Marzie., Metzker, M.Lee., Abramzon, S., Adams, C., Alder, J., Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D., Anguiano, D., Anguiano, D., Anguiano, D., Anguiano, D., Anguiano, D., Banderanaike, D., Barder, M., Barnstead, M., Benahmed, F., Biddwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F., Biddwin, D., Bandaranaike, D., Barrell, K., Calderon, E., Carderon, E., Carderon, E., Carderon, E., Carder, C., Corkrell, R., Cox, C., Coyle, M., Cree, A., D. Kouza, L., Davis, C., Davis, C., Deramo, C., Ding, Y., Dinh, H., Divya, K., Davis, C., Davis, C., Deramo, C., Ding, Y., Dinh, H., Divya, K., Davis, C., Davis, C., Deramo, C., Evelsand, C., Davis, C., Deramo, C., Falls, T., Falls, T., Falls, T., Falls, M., Egan, A., Escotto, M., Eugene, C., Evans, C.A., Falls, T., Falls, T., Falls, M., Gebregeorgis, E., Geer, K., Gill, R., Grady, M., Guevara, W., Gebregeorgis, E., Geer, K., Gill, R., Grady, M., Garer, M., Gebregeorgis, E., Geer, K., Gill, R., Grady, M., Hendardez, R., Hines, S., Hladun, S.L., Hodgson, A., Hogues, M., Harvey, Y., Havlak, P., Hawes, A., Henderson, N., Hernandez, R., Karpathy, S., Kelly, S., Kally, L., Mandes, J., Johnson, R., Mandelbard, L., Loulseged, H., Lovan, J., Lewis, L., Liu, W., Liu, Y., Liu, W., Liu, Y., Martin, K., Martin, R., Martinez, R., Manden, M., Malloy, K., Manden, M., Malloy, K., Mangum, B., Manden, M., Martin, R., Popori, C., Neal, D., Newton, V., Robe, R., Popori, C., L., Popori, C., Neal, D., Newton, V., Robe, R., Reger, R., Reger, R., Reige, F., Rickey, R., Relly, R.
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245104 bp DNA linear 'HTG 15-NOV-2002
Rattus norvegicus clone CH230-129P3, WORKING DRAFT SEQUENCE, 3
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Rodentia, Sciurognathi, Muridae, Murinae,
                                                                  CCAAAGTGCAGGGAGATAATGAGAAAACAATGGACAAAAGTACTGAAAAAGACAAAAAG
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773 GAATGGTTTCACTTTTCATGTGTTTCACTTACCTATAAACCAAAGGGGAAATGGTATTGC
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HTG; HTGS_PHASE1; HTGS_DRAFT; I
Rattus norvegicus (Norway rat)
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Best Local Similarity
Matches 744; Conserv
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Morley, K.C.

Direct Submission

AL Submission

AL Submitted (19-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

Stat Genome Sequencing Consortium.

Stat Genome Sequencing Consortium.

Direct Submission

AL Submitted (15-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

ON NOV 15, 2002 this sequence version replaced gi:23265010.

The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Esch contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature
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NOTE: This is a "working draft' sequence It currently consists of 3 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N. but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
Shetty,J., Shvartsbeyn,A., Sisson,I., Sitter,C.D., Smajs,D., Sneed,A., Sodergren,E., Song,X.-Z., Sorelle,R., Sosa,J., Steimle,M., Strong,R., Sutton,A., Svatek,A., Tabor,P., Taylor,C., Taylor,T., Thomas,N., Thomas,S., Tingey,A., Trejos,Z., Usmani,K., Valas,R., Vera,V., Villasana,D., Waldron,L., Walker,B., Wang,Q., Wang,S., Warren,B., Waldron,L., Walker,B., Wang,J., Williams,G., Willson,R., Wleczyk,R., Wooden,H., Worley,K., Wright,D., Wright,R., Wu,J., Yakub,S., Yen,J., Yoon,L., Yoon,V., Yu,F., Zhang,J., Zhou,J., Zhou,X., Zhao,S., Dunn,D., von Niederhausern,A., Weiss,R., Smith,D.R., Holt,R.A., Smith,H.O., Weinstock,G. and Gibbs,R.A.
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32 241782: gap of unknown length
33 242944: contig of 1162 bp in length
52 243044: gap of unknown length
15 245104: contig of 2060 bp in length.
Location/Qualifiers
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/mol_type="genomic DNA"

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45075 c 46272 g 57482 t 38750 others
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Pred. No. 1.3e-136;
); Mismatches 77;
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                                               extension
                                                                                                                                      end sequence:BH310917"
240971. .241683
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/clone="CH230-129P3"
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/note="wgs_end_e
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DEFINITION ACCESSION VERSION KEYWORDS

AC094539/c

RESULT 15

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SOURCE ORGANISM

REFERENCE AUTHORS

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Direct Submission

Submitted (109-MAY-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

On May 9, 2003 this sequence version replaced gi:24942175.

The sequence in this assembly is a combination of BAC based reads and whole genome shocgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, by sized gaps filled with NB to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome table.
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Submitted (15-SEP-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA (bases 1 to 247796).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Consensus quality: 228486 bases at least Q40
Consensus quality: 232830 bases at least Q30
Consensus quality: 235433 bases at least Q20
Estimated insert size: 233865, sum-of-contigs estimation
Quality coverage: 6x in Q20 bases; sum-of-contigs estimation
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1 247796: contig of 247796 bp in length.
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/note="wgs_contig"
68374 a 51336 c 52193 g 65763 t 10130 others
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Center code: BCM
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/mol_type="genomic DNA"
/db_xref="taxon:10116"
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Center clone name: CH230-419
-------- Summary Statistics
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Mizzny, Dandzren, Matsherooks, S., Amin, N., Anguiaho, D., Allen, H., Alsberooks, S., Amin, N., Anguiaho, D., Bandaranake, D., Barber, M., Baca, E., Baden, H., Baladrin, D., Bandaranake, D., Barber, M., Barnstead, B., Barnstead, B., Barnstead, B., Barnstead, B., Brown, M., Bardwin, D., Bandaranake, D., Barber, M., Barnstead, B., Brown, M., Bardwin, D., Carter, K., Cavazo, I., Ceasar, H., Cener, A., Usur, C., Cardens, V., Carter, K., Cavazo, I., Ceasar, H., Cener, J., Chu, J., Chacko, C., Cave, M., Chen, Z., Chu, J., Chacko, C., Cave, M., Chen, J., Chu, J., Chacko, C., Cave, M., Chen, J., Chu, J., Chacko, C., Dang, M., Cree, M., Divala, M., Chacko, D., Danson, S., Deramo, C., Ding, Y., Dinh, H., Davya, K., Danger, J., Dann, A., Dutchin, K., Duval, B., Eave, K., Bernandez, S., Filly, M., Cante, R., Carter, M., Cante, T., Falls, T., Fand, C., Ferrandez, S., Filly, M., Cante, R., Carter, M., Gabris, A., Cante, R., Carter, M., Gabris, A., Cante, R., Carter, M., Gabris, A., Cante, R., Carter, M., Gabris, M., Garter, M., Hamil, C., Hamilton, C., Hamilton, K., Havalk, E., Hawes, A., Henderson, N., Hermandez, J., Liu, J., Liu, M., Liu, Y., Liang, H., Johnson, B., Johnson, R., Mangum, B., Martin, K., Martin
                                                                                                                                                                                                                                                                  DNA linear HTG 09-MAY-2003
*** SEQUENCING IN PROGRESS ***.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae;
                               AC094539.6 GI:30466722
HTG; HTGS_PHASE2; HTGS_DRAFT; HTGS_ENRICHED.
Rattus norvegicus (Norway rat)
                                                                                                                                                                                                                                                                  AC094539 247796 bp
Rattus norvegicus clone CH230-419,
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Mammalia; Eutheria; Rodentia;
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Direct Submission
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216779 GACAAATCCAAGATTCCAGTCAACCCGAAAGATTCTTCCAGAAGACCTCGAAGACAG 216720
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GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.	OM protein - nucleic search, using frame_plus_p2n model Run on: January 12, 2004, 19:31:18; Search time 281 Seconds (without alignments)	3460.255 Million cell updates/sec Title: US-09-513-365A-1 Perfect score: 1481 Sequence: 1 MLGQQQQLYSSAALLTGERDNEKTWDKSTEKTKKDRRSR 280	Scoring table: BLOSUM62 Xgapop 10.0 , Xgapext 0.5 Ygapop 10.0 , Ygapext 0.5 Fgapop 6.0 , Fgapext 7.0 Delop 6.0 , Delext 7.0	Searched: 2276164 segs, 1736306516 residues	4 length: 0	Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries	Command line parameters: -WODEL=frame+_pzn, model -DEV=xlp -Q=/cgnZ_1/USFTO_spool_p/US09513365/runat_12012004_163934_28802/app_query.fasta_1.455 -Q=/cgnZ_1/USFTO_spool_p/US09513365/runat_12012004_163934_28802/app_query.fasta_1.455 -DB=PublishedA AppliLations NA -OFWFM=fastagp_SUFFIX=p2n.rnpb -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MXX=100 -TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MXX=100 -MAX.En=200000000 -USER=LOCAL -OUTFWT=pto -NORM=ext -HEAPSTZE=500 -MINLEN=0 -NORDU-6 -CICPD=3 -NO MMAP -LARGEQUERY -NOS SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7	Database: Published Applications NA:* 1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:* 2: /cgn2_6/ptodata/2/pubpna/PCT_NEW PUB.seq:* 3: /cgn2_6/ptodata/2/pubpna/US06_NEW PUB.seq:* 4: /cgn2_6/ptodata/2/pubpna/US06_NEW PUB.seq:*	5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:* 6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:* 7: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:* 8: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:* 9: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:* 10: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:* 11: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:* 12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:* 13: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:* 14: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:* 15: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:* 16: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:* 16: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:* 16: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:* 17: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:* 18: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:* 18: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*	Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. SUMMARIES Result Query No. Score Match Length DB ID Description

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GENERAL INFOGENERALION:
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TITLE OF INVENTION: Human TSC403 gene and hum
FILE REFERENCE: 060193
CURRENT PAPLICATION NUMBER: US/10/115,899
CURRENT FILING DATE: 2002-04-05
PRIOR APPLICATION NUMBER: US/601,478
PRIOR FILING DATE: 2000-08-03
PRIOR FILING DATE: 1998-04-28
PRIOR FILING DATE: 1998-04-28
PRIOR FILING DATE: 1998-03-05
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     166 MetAlaAsnGlyIleGluAspCysAspAspGlnProProLysGluLysLysSerLysSer 185
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      616 CCCATCGACCCCAACGAACCCACGTACTGTCTGTGCAACCAGGTCTCCTATGGGGAGATG 675
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  736 AATCATAAACCCAAGGGCAAGTGGTACTGTCCCAAGTGCCGGGGGGGAGAAGAGGAGAAGACC 795
                                                                                                                                                                                                                                        25 GGGGAGCAGCTCCACCTGGTGAAC---TATGTGGAGGACTACCTGGACTCCATCGAGTCC 81
                                                                                                                                                                                                                    LeuProHisAspMetGlnArgAsnValSerValLeuArgGluLeuAspAsnLysTyrGln 57
                                                                                                                                                                                                                                                                                              GluThrLeuLysGluIleAspAspValTyrGluLysTyrLysLysGluAspAspLeuAsn 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18 GlyGluArgSerArgLeuLeuThrCysTyrValGlnAspTyrLeuGluCysValGluSer
                                                                                                                                                                                                                                                                                                                                                                         GlnLysLysArgLeuGlnGlnLeuLeuGlnArgAlaLeuIleAsnSerGlnGluLeuGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         226 IleGlyCysAspAsnGluGlnCysProIleGluTrpPheHisPheSerCysValSerLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       246 Thr Tyr Lys ProLys Gly Lys Trp Tyr Cys ProLys Cys Arg Gly Asp Asn Glu Lys Thr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              206 AlaileAspProAsnGluProThrTyrCysLeuCysAsnGlnValSerTyrGlyGluMet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  118 MetGluLeuHisSerGlnCysPheGlnAspProAlaGlu------
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TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PC005
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                                                                                                US-09-513-365A-1 (1-280) x US-09-968-653A-4 (1-873)
                      Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-764-877-3454
; Sequence 3454, Application US/09764877
; Patent No. US20020147140A1
; GENERAL INFORMATION:
  75.74%
59.19%
57.63%
    Similarity:
cal Similarity:
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DB:
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181 LyslysSerlysSerAlaLyslysLysLysArgSerLysAlaLysGlnGluArgGluAla
                          692 TCACCTGTTGAGTTTGCAATAGATCCTAATGAACCTACATACTGCTTATGCAACCAAGTG
                                                                                                                                                                                                                                  SerCysValSerLeuThrTyrLysProLysGlyLysTrpTyrCysProLysCysArgGly
                                                                                                                                                                                                                                                                        TCATGTGTTTCACTTACCTATAAACCAAAGGGGAAATGGTATTGCCCAAAGTGCAGGGGA
                                                                                                                                                                                                                                                                                                            AspAsnGluLysThrMetAspLysSerThrGluLysThrLysLysAspArgArgSerArg
                                                                                                                                                                                                                                                                                                                                       GATAATGAGAAAACAATGGACAAAAAGTACTGAAAAAGACAAAAAAGGATAGAAGATCGAGG
                                                                          SerProValGluPheAlaIleAspProAsnGluProThrTyrCysLeuCysAsnGlnVal
                                                                                                                                                       SerTyrGlyGluMetIleGlyCysAspAsnGluGlnCysProIleGluTrpPheHisPhe
                                                                                                                                                                                           rcriaridegeadardardegargreacaargaacagrerccaarreaargerrrcacrrr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Garkavstev, Igor
Riabowol, Karl
TITLE OF INVENTION: p3.1NG1 as a Mediator of p53 Signaling
Pathway
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/968,653A
FILING DATE: 01-Oct-2001
CLASSIFICATION: <UNknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    873
161
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/006,783A
FILING DATE: 15-JAN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REGISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 97,837
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 300 South Wacker Drive
CITY: Chicago
STATE: Illinois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; SEQUENCE DESCRIPTION: SEQ ID NO:
US-09-968-653A-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 4, Application US/09968653A Publication No. US20030073084A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: 312-913-0001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Gudkov, Andrey V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 873 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 312-913-0002
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
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853.50
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Pred. No.:
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CTGGGCGACGAGAAGATCCAGATCGTGAGCCAGATGGTGGAGCTGGAGGAGAACCGCACG 369
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ------SerGluArgAlaSerAspLysAlaLysMetAspSerSer 143
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 76 LeuAsnGlnLysLysArgLeuGlnGlnLeuLeuGlnArgAlaLeuIleAsnSerGlnGlu 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    310 CGGCAGGTGGACAGCCACGTGGAGCTGTTCGAGGCGCAGCAGGAGCTGGGCGACACAGTG
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                 Riabowol, Karl
TITLE OF INVENTION: p33/ING1 as a Mediator of p53 Signaling
Pathway
                                                                                                                                                                             CUMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: ISH PC compatible

OPERATION SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/968,653A

FILING DATE: 01-Oct-2001

CLASSIFICATION **CURROWN>

PRIOR APPLICATION NUMBER: US/09/006,783A

FILING DATE: 15-JAN-1998

ATTORNY AGENT INFORMATION:

NAME: NO. US200330073084Alman, Kevin E

REGISTRATION NUMBER: 35,303

REGISTRATION NUMBER: 35,303
                                                                                                   & Berghoff
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 116 ArgGlnMetGluLeuHisSerGlnCysPheGlnAspProAlaGlu-
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135
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Matches:
Conservative:
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                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: McDonnell Boehnen Hulbert
STREET: 300 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches:
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LOCATION: 16..897
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
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TELEPHONE: 312-913-0001
TELEFAX: 312-913-0002
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 2061 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4.91e-72
722.00
74.36%
57.69%
                                                                                                                                  CITY: Chicago
STATE: Illinois
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear MOLECULE TYPE: CDNA
                                                                   NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Percent Similarity:
Best Local Similarity:
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DB:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6652 AAGAAGAGGCTCCAAGGCCAAGGCGAGGGGAGGCGTCCCCTGCCGACCTCCCCATC 6711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6712 GACCCCAACGAACCCACGTACTGTGTGCAACCAGGTCTCCTATGGGGAGATGATCGGC 6771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98 AspGluLysIleGlnIleValThrGlnMetLeuGluLeuValGluAsnArgAlaArgGln 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            168 AsnGlyIleGluAspCysAspAspGlnProProLysGluLysLysSerLysSerAlaLys 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                208 AspProAsnGluProThrTyrCysLeuCysAsnGlnValSerTyrGlyGluMetIleGly 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CysAspAsnGluGlnCysProlleGluTrpPheHisPheSerCysValSerLeuThrTyr 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LysProLysGlyLysTrpTyrCysProLysCysArgGlyAspAsnGluLysThrMetAsp 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           118 MetGluLeuHisSerGlnCysPheGlnAspProAlaGlu---SerGluArgAlaSerAsp 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           137 LysAlaLysMetAspSerSerGlnPro------GluArg 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LysLysLysArgSerLysAlaLysGlnGluArgGluAlaSerProValGluPheAlaile 207
                                                                                                                                                                                                                                                                                                                                                                                       97
                                                                                                                                                                                                                                                                                                                       58 GluThrieuLysGluIleAspAspValTyrGluLysTyrLysLysGluAspAspLeuAsn
                                                                                                                                                                                                                                                                                                                                                                                       78 GlnLysLysArgLeuGlnGlnLeuLeuGlnArgAlaLeuIleAsnSerGlnGluLeuGly

    refer to PALM or file wrapper

                                                                                                                                                                     Length:
Matches:
Conservative:
                                                                                                                                                                                                                                                                                      US-09-513-365A-1 (1-280) x US-09-764-877-3454 (1-8487)
                                                                                                                                                                                                                     Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LysSerThrGluLysThrLysLysAspArg 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 2, Application US/09968653A; Publication No. US20030073084A1; GENEAL INFORMATION: APPLICANT: Gadkov, Andrey V
Prior application data removed - NUMBER OF SEQ ID NOS: 4031
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 3454
LENGTH: 8487
TYPE: DNA
ORGANISM: Homo sapiens
US-09-764-877-3454
                                                                                                                                                                 7.72e-72
728.00
75.22$
59.13$
49.16$
                                                                                                                                                                                                      Percent Similarity:
Best Local Similarity:
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US-09-968-653A-2
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                                                                                                                                                                                                                                                                                                                       13 GTGCAGCGCGCGCTGATCCGCAGCCAGGAGCTGGGCGACGAGAAGATCCAGATCGTGAGC 72
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Publication No. US/0030073623A1
GENERAL INFORMATION:
APPLICANT: Hyear, Inc.
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
TITLE OF INVENTION: ROW VARIOUS CDNA LIBRARIES
FILE REPERENCE: 20411-756
CURRENT APPLICATION NUMBER: US/09/918,995
CURRENT FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: US/09/235,076
PRIOR FILING DATE: 1999-01-20
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125
23
36
14
2
                                                                                                                                          Matches:
Conservative:
Mismatches:
Indels:
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                                 LOCATION: 1..630
SEQUENCE DESCRIPTION: SEQ ID
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662.00
75.49%
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Best Local Similarity:
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                                                                                                          Alignment Scores:
FEATURE:
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              GlnProGluArgSerSerArgArgProArgArgGlnArgThrSerGluSerArgAspLeu
                                                490 AAGĆĆĆ-----AACAĞÇAAGČĞTCAČĞGĞĞĞĞĞĞĞĞĞĞAACAACĞAĞAACYCGTGAGAAC
                                                                                  CysHisMetAlaAsnGlyIleGluAspCysAspAspGlnProProLysGluLysLysSer
                                                                                                                 544 GCGTCCAGCAACCACGACGACGACGCGCCTCGGGCACACCCAAGGAGAAGAAGGACC
                                                                                                                                                        LysSerAlaLysLysLysLysArgSerLysAlaLysGInGluArgGluAlaSerProVal
                                                                                                                                                                             GluMetIleGlyCysAspAsnGluGlnCysProIleGluTrpPheHisPheSerCysVal
                                                                                                                                                                                                                                                                                                                         784 GGGCTCAATCATAAACCCAAGGGCAAGTGGTACTGTCCCAAGTGCCGGGGGGAAGAACGAG
                                                                                                                                                                                                                             204 GluPheAlaileAspProAsnGluProThrTyrCysLeuCysAsnGlnValSerTyrGly
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Riabowol, Karl
TITLE OF INVENTION: p33/ING1 as a Mediator of p53 Signaling
Pathway
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/968,653A
FILING DATE: 01-Oct-2001

CLASSIFICATION: CUNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSE: McDonnell Boehnen Hulbert & Berghoff
STREET: 300 South Wacker Drive
CITY: Clasgo
STATE: 111,nois
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAGACCATGGACAAAGCCCTGGAGAAATCCAAAAAAGAGAGG 885
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APPLICATION NUMBER: US/09/006,783A
FILING DATE: 15-JAN-1998
ATTORNEY/ABOUT INFORMATION:
NAME: NO. US20030073084Alnan, Kevin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REGISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 97,837
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 6, Application US/09968653A Publication No. US200300730B4A1 GENERAL INFORMATION: APPLICANT: Gudkov, Andrey V
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TYPE: nucleic acid
STRANDEDNESS: single
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Percent Similarity:
Best Local Similarity:
                       Alignment Scores:
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                                                                                                                                                              421
85
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10
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                                                                                                                                                             Length:
Matches:
Conservative:
Mismatches:
Indels:
SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 37033 LENGTH: 421
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US-10-117-722-435
Sequence 435, Application US/10117722
Publication No. US20030219744A1
GENERAL INFORMATION:
APPLICANT: Tang, Y. Tom
APPLICANT: Liu, Chenghua
                                                                                                               Ö
                                                                                        NAME/KEY: misc feature
LOCATION: (1)...(421)
OTHER INFORMATION: n = A,T,C or
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474.00
90.00$
85.00$
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; LOCATION: (164)..(1420)
US-10-117-722-435
                                                         TYPE: DNA ORGANISM: Homo sapiens FEATURE:
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ORGANISM: Homo sapiens
                                                                                                                                                                               Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       563 AACAATCACCATGCTCATTCACATACTCCAGTGGAAAAAGGAAATATAATCCAACTTCT 622
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 623 CACCATACGACAACAGATCATATTCCTGAAAAGAAATTTAAATCTGAAGCTCTTCTATCC 682
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             803 GGCTCGTTATCTTCAGGAACTGGTGCAGGGGCAATTACCATGGCAGCTGCTCAAGCAGTT 862
                                                                                                                                                                                                                                                                                                      42 MetGlnArgAsnValSerValLeuArgGluLeuAspAsnLysTyrGlnGluThrLeuLys 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          81 ------ArgLeuGlnGlnLeu-----LeuGlnArgAlaLeuIleAsnSerGln 94
                                                                                                                                                                                                                                                                                                                                443 TTGAGAAAGCTGGATCAGGAACTGGCTAAGTTAAAATGGAGCTGGAAGCTGATAATGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22 ArgleuLeuThrCysTyrValGlnAspTyrLeuGluCysValGluSerLeuProHisAsp
                                                                                                                                                                                                                                                                                                                                                                                                  62 GluileAspAspValTyrGluLysTyrLysLysGluAspAspLeuAsnGlnLysLys---
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    1864
102
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198
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    Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                   US-09-513-365A-1 (1-280) x US-10-117-722-435 (1-1864)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              135 ------SerAspLysAlaLys-------
                                                                                              Indels:
                                                                                                                         Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        134 -----
1.03e-30
359.00
34.22%
22.52%
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Pred. No Score: Percent Best Loc Query Mai	.: Simil al Si tch:	arity: .milarity:	1.03e-30 359.00 34.22* 22.52* 24.24*	Length: Matches: Conservative: Mismatches: Indels: Gaps:	1864 102 53 59 198 11	
US-09-51	3-365A	1-1 (1-280)) x US-10-037-2	70-435 (1-1		
ò	22	ArgLeuLeu 	gLeuLeuThrCysTyrValGln	nAspTyrLeuGluCysValGlu:::	alGluSerLeuProHisAsp	41
Dβ	155	Addeccece	ATGTTGTACCTAGAA	GACTATCTGGAAATGA	абавссвсватеттвтасстававаетатстеваатвателейсавсттестатеват	214
δ	42	MetGlnArg	AsnValSerValLeu	ArgGluLeuAspAsnL	MetGlnArgAsnValSerValLeuArgGluLeuAspAsnLysTyrGlnGluThrLeuLys	19
Ob	215	CTGCGGGAC	cecttcacegaaate	GCCGAGATGGACCTGC	стессвевассветтся става в предоста в предос	271
ο,	62	GluIleAspA	AspValTyrGluLysTyrLysLy 	TyrLysLysGluAspAspL 	spLeuAsnGlnLysLys	80
Db	272		GATCAACTAGAACAA	GATCAACTAGAACAAAGAGTCAGTGAATTCTTTATGAATGCAAAGAA	TTATGAATGCAAAGAAAAT	322
λΌ	81	!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!	ArgleuGlnGln	nLeuLeuGlnA	nArgAlaLeulleAsnSerGln	94
ΩÞ	323	AAACCTGAG	CCTGAGTGGAGGGAAGAGCAAATGGCATC	ATGGCATCCATCAAAA	CATCAAAAAGACTACTATAAAGCTTTG	382
٥⁄	95	GluLeuGlyA	spGluLysIleGl	leValThrGlnM	euValG	114
QQ	383	GAAGATGCA	GATGAGAAGGTTCAG	::: TTGGCAAACCAGATAT		442
ò	115	AlaArgGln	etGluLeuHi	- A	aGluSerGluArgA	134
QQ	443	TTGAGAAAG	:::::::: TTGAGAAAGCTGGATCAGGAACTGGCTAAGT	::: GCTAAGTTTAAAATGG	::: TAAAATGGAGCTGGAAGCTGATAATGCT	502
δλ	134	1				134
Db	503	GGAATTACA	gaaatattagagagg	GGAATTACAGAAATATTAGAGGGGGATCTTTGGAATTAGACACTCCTTCACAG	CCAG	562
λ	134	1				134
Db	563	AACAATCAC	CATGCTCATTCACAT	CATGCTCATTCACATACTCCAGTGGAAAAAAGGAAATATAA	GGAAATATAATCCAACTTCT	622
۵,	134					134
QQ	623	CACCATACG	ACAACAGATCATATT	CCTGAAAAGAAATTTA	CCATACGACAGATCATATTCCTGAAAAGAAATTTAAATCTGAAGCTCTTTTATCC	682
λō	135		SerAspLysAlaLys		1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	139
qq	683	ACCCTTACG	CGTCAGATGCCTCTAAG	::: GATGCCTCTAAGGAAATACACTAGGTTGTCGAAATAATAAT	GTCGAAATAATACCACA	742
γ̈́ο	140	1 1 1 1 1 1		pSerSerGln	Pro	145
qa	743	GCCTCTTCT	 CTCTTCTAACAATGCCTACAATGTGAATTCCTC	GTGAATTCCTCCCAAC	 CTCTGGGATCCTATAACATT	802
ò	145					145
qa	803	GGCTCGTTA	TCTTCAGGAACTGGT	GCAGGGCAATTACCA	GGCTCGTTATCTTCAGGAACTGGTGCAGGGGCAATTACCATGGCAGCTGCTCAAGCAGTT	862
ò	146	GluArgSer	SerArgArgProArg	GluArgSerSerArgArgProArgArgGlnArgThrSerGlu	1u	159
qq	863	CAGGCTACA	GCTCAGATGAAGGAG	GGACGAAGAACATCAA	CAGGCTACAGCTCAGATGAAGGAGGAGGACGAAGAACATCAAGTTTAAAAGCCAGTTATGAA	922
<i>\</i> 5	159					159
Dp	923	GCATTTAAG	AATAATGACTTTCAG	TTGGGAAAAGAATTTT	GCATTTAAGAATAATGACTTTCAGTTGGGAAAAGAATTTTCAATGGCCAGGGAAACAGTT	982
ογ	160	Ser	SerArgAspLeuCysHisMetAl	MetAlaAsnGlyIleG	aAsnGlyIleGluAspCysAspAspGlnPro	177
QQ	983	GGCTATTCA	TCATCTTCGGCACTT	ATGACAACATTAACAC		1042
<i>\</i> 6	178	ProLysGlu	sGluLysLysSerLysSerAl	AlaLysLysLysLysA	SLysLysLysArgSerLysAlaLysGlnGlu	197
Db	1043	GCCGACTCA	CGGAGTGGTCGAAAG	AGCAAAAACAACAACA	GCCGACTCACGGAGTGGTCGAAAGAGCAAAAACAACAACAACAAGTCTTCAAGCCAGGAGTCA	1103

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                                                                                                                                                                                                  375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        77 AAATACCAAGAGATCCTGAAGGAGCTAGACGAGTGCTACGAGGGCTTCAGTCGCGAGAACA 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    95 GluLeuGlyAspGluLysIleGlnIleValThrGlnMetLeuGluLeuValGluAsnArg 114
115 AlaArgGlnMetGluLeuHisSerGlnCysPheGlnAspProAlaGlu---SerGluArg 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         55 LysTyrGlnGluThrLeuLysGluIleAspAspValTyrGluLysTyrLysLysGluAsp 74
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                                                                   196 GAGCTGGGCGACGAGAAGATCCAGATCGTGAGCCAGATGGTGGAGCTGGTGGAGAACCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        35 ValGluSerLeuProHisAspMetGlnArgAsnValSerValLeuArgGluLeuAspAsn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       75 AspieuAsnGlnLysLysArgLeuGlnGlnLeuLeuGlnArgAlaLeuIleAsnSerGln
                                                                                                               GluLeuGlyAspGluLysIleGlnIleValThrGlnMetLeuGluLeuValGluAsnArg
                                                                                                                                                                                                                                                                    AspLeuAsnGlnLysLysArgLeuGlnGlnLeuLeuGlnArgAlaLeuIleAsnSerGln
                                                                                                                                                                                                                                                                                                                                376 GACAAGCCCAACAGCAAGCGCTCACGGCGGCAGCAACAACGAGAACCGTGAG 429
                                                                                                                                                                                                                                                                                                               146 ---GluArgSerSerArgArgProArgArgGlnArgThrSerGluSerArgAsp
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; Sequence 146, Application US/09854133
; Publication No. US20020183499A1
; GENERAL INFORMATION:
; APPLICANT: Lodes, Michael J.
; APPLICANT: Mohamath, Raodoh
; APPLICANT: Henderson, Robert A.
; APPLICANT: Benson, Darin R.
; APPLICANT: Secrist, Heather
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
; TITLE OF INVENTION: THE THERAPY AND DIAGNOSIS OF LUNC
; FILE REFERENCE: 210121.475C10
; CURRENT APPLICATION NUMBER: US/09/854,133
; CURRENT FILING DATE: 2011-05-11
; NUMBER OF SEQ ID NOS: 735
; SEQ ID NOS: 735
; SEQ ID NO 146
; FILE METHOR COMPANIENT FALING DATE: 2011-05-11
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Matches:
Conservative:
Mismatches:
Indels:
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70.29%
49.28%
21.20%
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Best Local Similarity:
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                    17
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DB:
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No.:
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                                   1103 TCATCTTCCTCCTCCTCTTCCTTATCATCGTGTTCTTCATCATCAACTGTTGTACAA 1162
                                                                                                                                                                                                    245
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                                                                                                                                                                                                                                                                                                                                 GlyAspAsnGluLys-------ThrMetAspLysSerThrGluLysThr 273
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                                                                                                                                                                                                                                                                 246 ThrTyrLy8Proly8GlyLy8TrpTyrCy8ProLy8Cy8---------Arg
                                                                                                                                                                                                  226 IleGlyCysAspAsnGluGlnCysProIleGluTrpPheHisPheSerCysValSerLeu
                                                                     SerProValGluPhe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 146, Application US/09738973

Sequence 146, Application US/09738973

Parent No. US2002010563A1

GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Henderson, Robert A.
APPLICANT: Hing, Steven P.
APPLICANT: Aling, Steven P.
APPLICANT: Algate, Paul A.
APPLICANT: Algate, Paul A.
APPLICANT: Blaide, Machaer
APPLICANT: Blaide, Mark
APPLICANT: Bliot, Mark
APPLICANT: Ralos, Michael D.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
TITLE REFERENCE: 210121.475C9
CURRENT APPLICANTS
NUMBER OF SEQ ID NOS: 587

SOFTWARER: FastSEQ for Windows Version 3.0
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Matches:
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Mismatches:
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ORGANISM: Homo sapien
      198 ArgGluAla--
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Best Local Similarity:
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Pred. No.:
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PLANTS, TRANSGENIC PLANTS CONTAINING
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         289 ATAGATAGTCATGTAAAACGACTTGATGATGTTGAATAATTTT-----GCAGAA 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     340 GATTTAAAGCAAGAGGAAAAATTCCACCAGACGAGCCCTCTGTTCTTCCTCCACTACCT 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               162 pLeuCysHisMetAlaAsnGlyIleGluAspCysAspAspGln-----ProProLysGl 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         180 uLysLysSerLysSerAlaLysLysLysLysArgSerLysAlaLysGlnGluArgGluAl 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    145 GGTAATGGTAATCATTACAATAATGGTGGTCTTGATGAAGAGGAAAACGATTGAGAAAATG 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----ProGluArgSerSerArgArg-ProArgArgGlnArgThrSerGluSerArgAs 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27 TyrValGlnAspTyrLeuGluCysValGluSerLeuProHisAspMetGlnArgAsnVal 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25 TATGITGATGATTACCTTGAGTATGCAAGCACTTTCCCTGCAGAGTACTATACTA 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         54 ------AsnLysTyrGlnGluThrLeuLysGluIleAspAspValTyrGluLysTyr 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 71 LysLysGluAspAspLeuAsnGlnLysLysArgLeuGlnGlnLeuLeuGlnArgAlaLeu 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   232 ---AATGCGTTAAGTTTGTGTACCGAGAAGGTTTTATTGGCCCGACAAGCGTATGATCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     111 ValGluAsnArgAlaArgGlnMetGluLeuHisSerGlnCysPheGlnAspProAlaGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           91 IleAsnSerGlnGluLeuGlyAspGluLysIleGlnIleValThrGlnMetLeuGluLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            460 GATTATAGAGATAGAGACTGGGATCGT-GACAGGGATTTTGAGCTCATGCCTCCT----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               131 SerGluArgAlaSerAspLysAlaLysMetAspSerSerGln----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative:
Mismatches:
Indels:
                                                                                APPLICANT: HEDET, Jeff
APPLICANT: Kreps, Joel
APPLICANT: Wang, Xun
APPLICANT: Wang, Xun
APPLICANT: Wang, Xun
APPLICANT: Zhu, Tong
TITLE OF INVENTION: STRESS-REGULATED GENES OF PLA
TITLE OF INVENTION: SAME, AND METHODS OF USE
FILE REFERENCE: SCRIP1300-3
CURRENT APPLICATION NUMBER: US/09/938,842A
CURRENT FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: US 60/227,866
PRIOR PILING DATE: 2001-08-4
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR PLING DATE: 2001-01-6
PRIOR FILING DATE: 2001-01-6
PRIOR FILING DATE: 2001-01-6
PRIOR FILING DATE: 2001-01-6
PRIOR PLING DATE: 2001-01-6
PRIOR PLING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 5379
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Matches:
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                              US/09938842A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Arabidopsis thaliana
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45.35%
29.84%
18.74%
                          Sequence 1178, Application
Patent No. US20020160378A1
GENERAL INFORMATION:
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Best Local Similarity:
       US-09-938-842A-1178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-938-842A-1178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
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DB:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              196 GAGCTGGGCGACGAGAAGATCCAGATCGTGAGCCAGATGGTGGAGCTGGTGGAGAACCGC 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           115 AlaArgGlnMetGluLeuHisSerGlnCysPheGlnAspProAlaGlu---SerGluArg 133
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                                                                                                   146 ---GluArgSerSerArgArgProArgArgGlnArgThrSerGluSerArgAsp 162
                                                                                                                                                                                         376 GACAAGCCCAACAGCACACGCGCTCACGCGCGCGCCAACAACGAGAACCGTGAG 429
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                                                                                                                                                                                                                                                                                          Sequence 146, Application US/10144649A

Publication No. US20030118599A1

GENERAL INFORMATION:

APPLICANT: Lodes, Michael J.

APPLICANT: Wang, Tongtong

APPLICANT: Mang, Tongtong

APPLICANT: Algate, Paul A.

APPLICANT: Algate, Paul A.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR

TITLE OF INVENTION: THE THERAPY AND DIAGNOSIS OF LUNG CANCER

FILE REFERENCE: 210121.475C11

CURRENT APPLICATION NUMBER: US/10/144,649A

CURRENT APPLICATION NUMBER: US/10/144,649A

NUMBER OF SEQ ID NOS: 749

SOFTWARE: FastSEQ for Windows Version 3.0

SECTION 146
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Matches:
Conservative:
Mismatches:
Indels:
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70.29%
49.28%
21.20%
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ORGANISM: Homo sapien
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Best Local Similarity:
Query Match:
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US-10-144-649A-146
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Sequence 6348, Application US/10032585
Publication No. US20030180953A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Perry, Roemer D.
APPLICANT: Bo, Jiang
APPLICANT: Bo, Jiang
APPLICANT: Howard, Bussey
TITLE OF INVENTION: Gene Disruption Methodologies for Drug Target Discovery
FILE REFREENCE: 10182-005-999
CURRENT APPLICATION NUMBER: US/10/032,585
CURRENT FILING DATE: 2001-12-20
                                                                                                                                   :::||||||
310 TTAGAATTGGCGTATGAAGTCGCAATCAAGAACACAGAAATTCCTAGAGGTTTAAGACTG 369
                                                                                                                                                                                                                                                                                        AAATCAAACAGCAAATCGTCGCAGGCACTGAAGAGCGAATCAAGAAGAGAAGCCATGGCT 489
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                                                                                                                                                                                                                                                                                                                              ------ArgThrSerGluSerArg 161
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                                     AspGluLysIleGlnIleValThrGlnMetLeuGluLeuValGluAsnArgAlaArgGln 117
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211 AATATCAACAAGATTTATGAAGAACTGATGCCATCGCTG-
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SOFTWARE: PatentIn version 3.1
                                                                                                             MetGluLeu-----
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ORGANISM: Candida albicans
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LENGTH: 897
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APPLICANT: Summers, Eric
IITLE OF INVENTION: Methods for Improving Secondary Metabolite Production in Fungi
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                                                                                                                                                                 597 GGTGTCCTTTGGAGACATGATTGCCTGTGACAATGAGAATTGCCAAGGAGGTGAATGGTT 656
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                                                        200 aSerProVal --- GluPheAlaIleAspProAsnGluProThrTyrCysLeuCysAsnGl
                                                                                            537 TATGCCAATTGAAGAGCAGCCAATCGATCCAAACGAACCAACTTACTGTGTCTGCCATCA
                                                                                                                               nValSerTyrGlyGluMetIleGlyCysAspAsnGluGlnCysPro---IleGluTrpPh
                                                                                                                                                                                                                          eHisPheSerCysValSerLeuThrTyrLysPro-----LysGlyLysTrp 253
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Mismatches:
Indels:
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Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILE REFERENCE: 109272.147

CURRENT APPLICATION NUMBER: US/09/801,368

CURRENT FILING DATE: 2001-03-07

PRIOR FILING DATE: 2000-01-19

PRIOR PELING DATE: 2000-01-19

PRIOR PELING DATE: 1999-10-20

PRIOR FILING DATE: 1999-10-20

NUMBER OF SEQ ID NOS: 440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Milne, Todd
No. US20020128250Alman, Thea
                                                                                                                                                                                                                                                                                                               Sequence 257, Application US/09801368 Patent No. US20020128250A1
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263.50
37.04%
23.15%
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Holtzman, Doug
Madden, Kevin
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Salama, Sofie
Sherman, Amir
                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Busby, Robert APPLICANT: Cali, Brian
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Maxon, Mary
Milne, Todd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                               US-09-801-368-257
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LENGTH: 993
                                                                                                                               219
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APPLICANT:
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US-10-032-	-585-6348				
Alignment S Pred. No.: Score: Percent Sim Best Local Query Match	Scores: : imilarity: l Similarity: ch:	4.38e-19 253.00 36.25% 25.38% 17.08%	Length: Matches: Conservative: Mismatches: Indels: Gaps:	897 84 36 108 104	
US-09-513-	-365A-1 (1-280	0) x US-10-032-	585-6348 (1-897)		
oy G	19 GluArgSeri ::: 4 GATACATCA	erArgLeuLeuThrCysTyrVal ::: CAACTGTACTTGAGAAATACACA	STYrValGlnAspTyrL ATACACAGGGAT	LeuGluCysValGluSerLeu 	38 51
ć	39 ProHisAsp	sAspMetGlnArgAsnVal	lSerValLeuArgGluL	LeuAspAsnLysTyrGlnGlu	58
QQ	52 CCACTIGAA	AGTGAGGCATTTATT	: AGAGGAAATCAAAAGC	::::::::::::::::::::::::::::::::::::::	111
λo.	9 ThrLeuLy	-		GlulleAspAsp	65
a	2 GCAAG	ACGATACCAAACTCG	TGACCATCAACTTCAT	aaatttatacgaacaaatggg	
λ Q	66 ValTyrGluLy 172 ACACTAACTAA	liystyflyslysglu ::: aacatccaaggaa	AspaspL GACCAGT	euAsnGlnLysLysArgLeuGlnGlnLeu 	85 213
λ	86 LeuGlnArg	nArgAlaLeuIleAsnSe	eAsnSerGlnGluLeuGlyAspGl	GluLysIleGlnIleValThr	105
qq	ATC	::: AGATATGAAGCTTGT		 ATTCTATTGGCTAA	7
ò	106 GlnMetLeu	euGluLeuValGluAs	euValGluAsnArgAlaArgGlnMetGluLeuHi	GluLeuHisSerGlnCysPhe	125
දු අු	274 ACTGCATTG	 3TTTTTGATATCGAA	 actgcattgtttttgatatcgaacatctatatcattttgag	 GAG	315
λ̈́o	126 GlnAspProAl	oAlaGluSerGluArgAl	aSerAspLysA	LysMetAspSerSerGlnPro	145
qq	316		ACAGACATTGCC	CCAAGCTAGAAAGAGATGAATT-	347
δ	146 GluArgSer	rSerArgArgProAr	gArgGlnArgThrS	er-GluSerArgAspLeuCysHi	165
QΩ	348 GTTGCCTCC	CTTTAGAACACCCCA	TCGAGCTAACTGAAGT		407
<i>\</i> 6	165 sMetAlaAs	snGly11	eGluAspCysAspAspGlnProProLysGluLysLysS	oLysGluLysLysSerLysSe	185
QQ	408 ATCACTTAAT	-B	GTGCCTCTGCCACACC		467
ò	185 rAla			8LysLys	189
qq	468 GGCAACTCC	CAGTGGCAGAAACAG	TGAAAAGATCCAAAA	CTCCAGTGGCAGAAACAGTGAAAAAGATCCAAAAGAAAGTTAGTGTTAAAGG	527
ò	190	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1		LysArgSerLysAl	194
Ор	528 GGCGTCCTC	cricrcreecrcagr	cgtcctcttctctggctcagtcatcctctgcttcaagacaggtgaag	CGACTCCGGT	587
à	194 aLysGlnGl	sGlnGluArgGluAlaSerP	rovalGlu		204
Dp	588 AGAAGAGAT	ragaggatcctctac	 		647
λ̈́o	205	PheAlaIl	leAspProAsnGluProThr	oThr	213
අ .	648 AGCAATGAC	 GCATAAATAGTGCAG	 CAGATGCAAATGGTCC		707
&	214T	yrCygLeuCygAsnG	CysAsnGlnValSerTyrGlyGluMetIl	uMetIleGlyCysAspAsnGl	231
QQ	708 TAATCTATA	~[⊣	GTGTTTCATTTGGTGA	TGGTTC	797
ò	231 uGlnCysPr	rolleGluTrpPheH	isPheSerCysValSe	nCysProlleGluTrpPheHisPheSerCysValSerLeuThrTyrLysBroLysGl	251
Q	768 AGACTGTAP	agrargaricgrific	ATTGGAGTTGTGTTGG	GATCACATCACCTCCTAAAGA	827
ò	251 уЬув	TrpTyrCysProL	ysCysArgGlyAspAsı	${\tt TrpTyrCysProLysCysArgGlyAspAsnGluLysThrMetAspLysSe}$	269

qa	
ò	269 rThrGluLysThrLysLysAspArgArgSer 279
qa	864 GATGGAGAAAGAAAAGAAAGAAGAAC 894
Search cor Job time	Search completed: January 12, 2004, 19:54:49 Job time : 290 secs

